GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:22:25 ; Search time 67.39 Seconds
(without alignments)
135.198 Million cell updates/sec

Title: US-09-155-739-11
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....NYGVYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101:*
1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	655	100.0	123	16	AAR81323	Humanized VLA-4 an
2	655	100.0	142	16	AAR81333	Human VLA-4 reshap
3	655	100.0	142	18	AAW22428	Humanised alpha-4
4	648	98.9	123	18	AAW22413	Humanised alpha-4
5	552	84.3	123	16	AAR81330	Mouse anti-VLA-4 a
6	544	83.1	140	16	AAR81327	Mouse VLA-4 antibo
7	544	83.1	140	18	AAW22410	Alpha-4 integrin m
8	523.5	79.9	120	19	AAW44124	Heavy chain variab
9	523.5	79.9	431	22	AAB30693	A fusion of single
10	523	79.8	136	16	AAR76681	Human/murine chime
11	523	79.8	136	17	AAW04396	Chimaeric human/mu
12	523	79.8	269	16	AAR76682	Human ONS-M21 anti
13	523	79.8	269	17	AAW04397	Chimaeric human/mu
14	515	78.6	119	16	AAR81325	Humanized VLA-4 an
15	515	78.6	119	18	AAW22426	Humanised alpha-4
16	512	78.2	119	16	AAR81324	Humanized VLA-4 an
17	512	78.2	119	18	AAW22425	Humanised alpha-4
18	507.5	77.5	135	21	AAB07969	A heavy chain vari
19	504.5	77.0	118	14	AAR37611	hIL2R Ab H chain V
20	503	76.8	119	20	AAY52717	Humanised ATR-5 H
21	503	76.8	119	22	AAB74978	Humanised ATR-5 H
22	499	76.2	119	20	AAY52719	Humanised ATR-5 H
23	499	76.2	119	22	AAB74980	Humanised ATR-5 H
24	496	75.7	136	17	AAR92084	Humanised antibody
25	495	75.6	119	16	AAR81331	Human 2*CL antibod
26	493	75.3	119	20	AAY52718	Humanised ATR-5 H
27	493	75.3	119	22	AAB74979	Humanised ATR-5 H
28	492	75.1	117	15	AAR57476	CDR-grafted anti-R
29	492	75.1	117	17	AAR92079	Murine 1308F VH CD
30	492	75.1	136	15	AAR57481	Humanized 1308F VH
31	491	75.0	119	20	AAY52708	Humanised ATR-5 H
32	491	75.0	119	22	AAB74969	Humanised ATR-5 H
33	489.5	74.7	120	18	AAW27551	Human Ab heavy cha
34	489	74.7	119	20	AAY52720	Humanised ATR-5 H
35	489	74.7	119	22	AAB74981	Humanised ATR-5 H
36	487.5	74.4	120	15	AAR47491	Humanised anti-CD1
37	487	74.4	119	20	AAY52712	Humanised ATR-5 H
38	487	74.4	119	20	AAY52715	Humanised ATR-5 H
39	487	74.4	119	22	AAB74973	Humanised ATR-5 H
40	487	74.4	119	22	AAB74976	Humanised ATR-5 H
41	486	74.2	140	18	AAW21847	Humanised heavy ch
42	486	74.2	143	15	AAR59942	Anti-VLA4 rAb huma
43	484.5	74.0	139	14	AAR33953	gH1 variable domai
44	484.5	74.0	139	18	AAW29753	CDR-grafted humani
45	484.5	74.0	139	21	AAY56877	gH1 variable domai

ALIGNMENTS

RESULT 1
AAR81323
ID AAR81323 standard; Protein; 123 AA.
XX
AC AAR81323;
XX
DT 02-APR-1996 (first entry)
XX
DE Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.
XX
OS Mus musculus.
XX
PN WO9519790-A1.
XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating
PT inflammatory disease.
XX
PS Claim 11; Page 69; 105pp; English.

```
XX
CC   The sequence encodes the mouse antibody 21.6 heavy chain variable
CC   region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions
CC   are linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig L chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   for inhibiting adhesion of a leukocyte to an endothelial cell and
CC   for treating inflammatory diseases such as multiple sclerosis.  They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   123 AA;


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  Best Local Similarity   100.0%;  Pred. No. 4e-53;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Db       1 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyamdywgqgtlvt 120

Qy     121 VSS 123
           |||
Db     121 vss 123


RESULT   2
AAR81333
ID   AAR81333 standard; Protein; 142 AA.
XX
AC   AAR81333;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Human VLA-4 reshaped antibody 21.6 light heavy variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..19
FT                    /note= "signal peptide"
FT   Region           20..49
FT                    /note= "framework region 1"
FT   Region           50..54
FT                    /note= "complementarity determining region 1"
FT   Region           55..68
FT                    /note= "framework region 2"
FT   Region           69..85
FT                    /note= "complementarity determining region 2"
FT   Region           86..117
FT                    /note= "framework region 3"
FT   Region           118..131
FT                    /note= "complementarity determining region 3"
FT   Region           132..142
FT                    /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99894.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 11; 105pp; English.
XX
CC   The sequence represents the human reshaped antibody 21.6 heavy
CC   chain variable region against leukocyte adhesion molecule VLA-4.
CC   Cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ99889)
CC   regions are linked to human constant regions in the construction
CC   of a humanized antibody against VLA-4.  The 5' and 3' ends of the
CC   mouse cDNAs are modified using PCR primers (AAQ99895-98) and then
CC   subcloned into mammalian cell expression vectors containing human
CC   kappa or gamma-1 constant regions.  In the humanized heavy chain,
CC   amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR
CC   framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig H chain.  Plasmids encoding the
CC   chimeric antibodies are transfected into COS cells.  The humanized
CC   antibodies can be used to inhibit adhesion of a leukocyte to an
CC   endothelial cell and to treat inflammatory diseases such as multiple
CC   sclerosis.  They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis.  The antibodies can
CC   also be used for detecting VLA-4, for affinity purification or for
CC   generating anti-idiotype antibodies.
XX
SQ   Sequence   142 AA;


  Query Match             100.0%;  Score 655;  DB 16;  Length 142;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-53;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      20 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Db      80 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyamdywgqgtlvt 139

Qy     121 VSS 123
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Db     140 vss 142


RESULT   3
AAW22428
ID   AAW22428 standard; Protein; 142 AA.
XX
AC   AAW22428;
XX
DT   09-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL version Ha.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
```

```
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= Leader
FT   Protein         20..142
FT                   /label= Mat_protein
FT                   /note= "VH version Ha (Claim 25)"
FT   Region          20..49
FT                   /label= FR1
FT                   /note= "21/28'CL framework region 1"
FT   Region          50..55
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          55..67
FT                   /label= FR2
FT                   /note= "21/28'CL framework region 2"
FT   Region          68..85
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          86..117
FT                   /label= FR3
FT                   /note= "21/28'CL framework region 3"
FT   Region          118..131
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Region          132..142
FT                   /label= FR4
FT                   /note= "21/28'CL framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;    96WO-US18807.
XX
PR   21-NOV-1995;    95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones ST,  Leger OJ,  Saldanha J,  Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74789.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Fig 11; 107pp; English.
XX
CC   This polypeptide, designated Ha, comprises the heavy chain variable
CC   region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also
CC   AAW22413).  It is composed of complementarity determining regions from
CC   the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal
CC   antibody 21.6 and a modified human 21/28'CL framework.  It can be
CC   expressed in mammalian host cells following PCR amplification and
CC   mutagenesis of appropriate mouse and human DNA sequences.  The
CC   humanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury.  The humanised
CC   antibody has a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   142 AA;

  Query Match             100.0%;  Score 655;  DB 18;  Length 142;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-53;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      20 qvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqapgqrlewmgridpangytky 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      80 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyamdywgqgtlvt 139

Qy     121 VSS 123
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Db     140 vss 142


RESULT   4
AAW22413
ID   AAW22413 standard; Protein; 123 AA.
XX
AC   AAW22413;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VH Ha.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1..30
FT                   /label= FR1
FT                   /note= "21/28'CL framework region 1"
FT   Misc-difference 27..30
FT                   /note= "21/28'CL residues 27-30 are replaced by
FT                         those of MAb 21.6, involved in antigen
FT                         binding"
FT   Region          31..35
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          36..49
FT                   /label= FR2
FT                   /note= "21/28'CL framework region 2"
FT   Region          50..66
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          67..98
FT                   /label= FR3
FT                   /note= "21/28'CL framework region 3"
FT   Misc-difference 72
FT                   /note= "21/28'CL Arg-72 is substd. by Ala of mouse
FT                         21.6 VL, important in supporting the CDR2
FT                         loop"
FT   Region          99..112
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Region          113..123
FT                   /label= FR4
FT                   /note= "21/28'CL framework region 4"
XX
PN   WO9718838-A1.
```

XX
PD 29-MAY-1997.
XX
PF 21-NOV-1996; 96WO-US18807.
XX
PR 21-NOV-1995; 95US-0561521.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR WPI; 1997-297879/27.
XX
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS Claim 25; Fig 7; 107pp; English.
XX
CC This polypeptide, designated Ha, comprises the heavy chain variable
CC region (VH) of a humanised alpha-4 integrin antibody 21.6. It is
CC composed of complementarity determining regions (CDRs) from the VH
CC region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody
CC 21.6 and a modified human 21/28'CL framework. It can be expressed
CC in mammalian host cells following PCR amplification and mutagenesis
CC of appropriate fragments of mouse and human DNA sequences. The
CC humanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used
CC to produce a claimed humanised 21.6 antibody that is useful in the
CC manufacture of a medicament for treating asthma, atherosclerosis,
CC AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC arthritis, transplant rejection, graft versus host disease, tumour
CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC ischaemia, and acute leukocyte mediated lung injury. The antibody
CC may also be used in the affinity purification of alpha-4 integrin
CC for use as a vaccine or an immunogen. It is also useful for
CC generating idiotypic antibodies. The humanised antibody has a
CC half-life in the human circulation essentially equivalent to that
CC of naturally occurring human antibodies.
XX
SQ Sequence 123 AA;

Query Match 98.9%; Score 648; DB 18; Length 123;
Best Local Similarity 99.2%; Pred. No. 1.8e-52;
Matches 122; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db      61 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyandywgqgtlvt 120

Qy     121 VSS 123
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Db     121 vss 123
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RESULT 5
AAR81330
ID AAR81330 standard; Protein; 123 AA.
XX
AC AAR81330;
XX
DT 02-APR-1996 (first entry)
XX
DE Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.
XX
OS Mus musculus.
XX

FH Key Location/Qualifiers
FT Region 1..30
FT /label= FR1
FT /note= "mouse heavy chain variable framework region 1"
FT Region 31..35
FT /label= CDR1
FT /note= "mouse heavy chain variable complementarity determining region 1"
FT Region 36..49
FT /label= FR2
FT /note= "mouse heavy chain variable framework region 2"
FT Region 50..66
FT /label= CDR2
FT /note= "mouse heavy chain variable complementarity determining region 2"
FT Region 67..98
FT /label= FR3
FT /note= "mouse heavy chain variable framework region 3"
FT Region 99..112
FT /label= CDR3
FT /note= "mouse heavy chain variable complementarity determining region 3"
FT Region 113..123
FT /label= FR4
FT /note= "mouse heavy light chain variable framework region 4"
XX
PN WO9519790-A1.
XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating
PT inflammatory disease.
XX
PS Disclosure; Page 68; 105pp; English.
XX
CC The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain
CC variable region (without signal sequence). Cloned cDNA CDR sequences of
CC mouse 21.6 variable light and variable heavy regions are linked to human
CC constant framework regions of the REI antibody for the light chain and
CC the 2*CL antibody for the heavy chain in the construction of a humanized
CC antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC modified using PCR primers (See AAQ99895-98) and then subcloned into
CC mammalian cell expression vectors containing human kappa or gamma-1
CC constant regions. In the humanized light chain, amino acids L45, L49,
CC L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC acid present in the equivalent position of the mouse 21.6 Ig light
CC chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC cells. The humanized antibodies can be used to inhibit adhesion of a
CC leukocyte to an endothelial cell and to treat inflammatory diseases such
CC as multiple sclerosis. They can also be used in the treatment of stroke,
CC cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC used for detecting VLA-4, for affinity purification or for generating
CC anti-idiotype antibodies.
XX
SQ Sequence 123 AA;

Query Match 84.3%; Score 552; DB 16; Length 123;

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  Best Local Similarity   82.9%;  Pred. No. 1.2e-43;
  Matches  102;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

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           :||| |||||: |||||||:|| |||||||||||| |:| | | |||:|||||||||||||
Db       1 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||: ||||||||::|||::|||| |||||||:|||||||||||||||||||| ||
Db      61 dpkfqgkatitadtssntaylqlssltsedtavyfcaregyygnygvyamdywgqgtsvt 120

Qy     121 VSS 123
           |||
Db     121 vss 123


RESULT   6
AAR81327
ID   AAR81327 standard; Protein; 140 AA.
XX
AC   AAR81327;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light heavy variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /note= "signal peptide"
FT   Region          20..49
FT                   /note= "framework region 1"
FT   Region          50..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..68
FT                   /note= "framework region 2"
FT   Region          69..85
FT                   /note= "complementarity determining region 2"
FT   Region          86..117
FT                   /note= "framework region 3"
FT   Region          118..131
FT                   /note= "complementarity determining region 3"
FT   Region          132..140
FT                   /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99892.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 2; 105pp; English.
XX
CC   The sequence represents the mouse antibody 21.6 heavy chain variable
CC   region directed against leukocyte adhesion molecule VLA-4.  Cloned
CC   cDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are
CC   linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized heavy chain, amino acids H27,
CC   H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig H chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   to treat inflammatory diseases such as multiple sclerosis.  They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   140 AA;


  Query Match             83.1%;  Score 544;  DB 16;  Length 140;
  Best Local Similarity   82.6%;  Pred. No. 7.5e-43;
  Matches  100;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: |||||||:|| |||||||||||| |:| | | |||:|||||||||||||
Db      20 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||: ||||||||::|||::|||| |||||||:|||||||||||||||||||| ||
Db      80 dpkfqgkatitadtssntaylqlssltsedtavyfcaregyygnygvyamdywgqgtsvt 139

Qy     121 V 121
           |
Db     140 v 140


RESULT   7
AAW22410
ID   AAW22410 standard; Protein; 140 AA.
XX
AC   AAW22410;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Alpha-4 integrin mouse MAb 21.6 VH region.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= Leader
FT   Region          20..49
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          50..54
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          55..68
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          69..85
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          86..117
FT                   /label= FR3
FT                   /note= "framework region 3"
FT
```

```
FT   Region          118..131
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Region          132..140
FT                   /label= FR4
FT                   /note= "framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;    96WO-US18807.
XX
PR   21-NOV-1995;    95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones ST,  Leger OJ,  Saldanha J,  Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74760.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 18; Page 69-70; 107pp; English.
XX
CC   This polypeptide comprises the heavy chain variable region (VH) of
CC   mouse anti-alpha-4 integrin monoclonal antibody 21.6.  The
CC   complementarity determining regions (CDRs) of the 21.6 VH can be
CC   incorporated into a human 21/28'CL framework to produce a claimed
CC   humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6
CC   antibody that is used in the manufacture of a medicament for
CC   treating a disease selected from asthma, atherosclerosis, AIDS,
CC   dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury.  The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen.  It is also useful for
CC   generating idiotypic antibodies.  The humanised antibodies of the
CC   invention have a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   140 AA;
```

```
  Query Match             83.1%;  Score 544;  DB 18;  Length 140;
  Best Local Similarity   82.6%;  Pred. No. 7.5e-43;
  Matches  100;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: |||||||:|| |||||||||||| |:| | | |||:|||||||||||||
Db      20 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpeqglewigridpangytky 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||: ||||||||::|||::|||| |||||||:|||||||||||||||||||| ||
Db      80 dpkfqgkatitadtssntaylqlssltsedtavyfcaregyyygnygvyamdywgqgtsvt 139

Qy     121 V 121
           |
Db     140 v 140
```

```
RESULT   8
AAW44124
ID   AAW44124 standard; Protein; 120 AA.
XX
AC   AAW44124;
XX
DT   05-JUN-1998  (first entry)
XX
DE   Heavy chain variable region of humanised NR-LU-13 antibody NRX451.
XX
KW   Heavy chain; variable region; murine; mouse; human; cancer antigen;
KW   antibody; humanised; NR-LU-13; NRX451; cancer; diagnosis;
KW   treatment.
XX
OS   Mus sp.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          31..35
FT                   /note= "complementarity determining region 1"
FT   Region          50..59
FT                   /note= "complementarity determining region 2"
FT   Region          99..109
FT                   /note= "complementarity determining region 3"
XX
PN   WO9746589-A2.
XX
PD   11-DEC-1997.
XX
PF   06-JUN-1997;    97WO-US10074.
XX
PR   07-JUN-1996;    96US-0660362.
XX
PA   (NEOR-) NEORX CORP.
XX
PI   Graves SS,  Henry AH,  Hylarides MD,  Mallet RW,  Pedersen JT;
PI   Rees AR,  Renojm,  Searle SMJ;
XX
DR   WPI; 1998-042124/04.
XX
PT   Humanised antibody binds same human cancer antigen as antibody
PT   NR-LU-13 - useful for pre-targeting methods, conventional antibody
PT   therapy and immunodiagnosis
XX
PS   Example 1; Fig 4; 100pp; English.
XX
CC   The present sequence is the heavy chain variable region of the
CC   humanised murine anti-human cancer antigen antibody (Ab) NR-LU-13,
CC   NRX451.
CC   A novel humanised Ab (hAb) binds the antigen bound by NR-LU-13. The
CC   hAb, specifically NRX451, or its conjugates can be used for the
CC   manufacture of a diagnostic or medicament for cancer diagnosis or
CC   treatment. The hAb has reduced immunogenicity and toxicity in
CC   humans, but retains the ability to bind the NR-LU-13 antigen.
XX
SQ   Sequence   120 AA;
```

```
  Query Match             79.9%;  Score 523.5;  DB 19;  Length 120;
  Best Local Similarity   82.9%;  Pred. No. 4.9e-41;
  Matches  102;  Conservative    8;  Mismatches   10;  Indels    3;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||||||||||||||||||:||||||||| |:|||||||||| ||
Db       1 qvqlvqsgaevkkpgasvkvsckasgfnikdtymhwvrqapgqglqwmgridpangntkc 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |  |||||||||||| :||||||||||:|||||||:||      | :::|||||||||||
Db      61 dlsfqgrvtitadtsintaymelsslrsddtavyycsrevl---tgtwsldywgqgtlvt 117

Qy     121 VSS 123
           |||
Db     118 vss 120
```

```
RESULT   9
AAB30693
ID   AAB30693 standard; Protein; 431 AA.
XX
AC   AAB30693;
XX
DT   02-APR-2001  (first entry)
```

```
XX
DE   A fusion of single chain antibody/streptavidin.
XX
KW   Streptavidin; tumour cell; cancer; adenocarcinoma;
KW   hematological malignancy; huNR-LU-10; EGP40; EPCAM.
XX
OS   Synthetic.
OS   Streptomyces avidinii.
OS   Homo sapiens.
XX
PN   WO200075333-A1.
XX
PD   14-DEC-2000.
XX
PF   05-JUN-2000; 2000WO-US15595.
XX
PR   07-JUN-1999;   99US-0137900.
PR   03-DEC-1999;   99US-0168976.
XX
PA   (NEOR-) NEORX CORP.
XX
PI   Goshorn SC,  Graves SS,  Schultz JE,  Lin Y,  Sanderson JA,  Reno JM;
XX
DR   WPI; 2001-091213/10.
DR   N-PSDB; AAC86562.
XX
PT   New vector constructs for expressing genomic streptavidin fusion
PT   proteins which are useful for targeting tumour cells associated with
PT   cancer, e.g. adenocarcinomas -
XX
PS   Example 1; Fig 10; 100pp; English.
XX
CC   The present sequence encodes a fusion of the single chain antibody
CC   huNR-LU-10 and streptavidin. The antibody binds the antigen EGP40 or
CC   EPCAM. The fusion protein is expressed using vectors of the invention.
CC   The specification describes vector constructs for expressing streptavidin
CC   fusion proteins. The vector comprises a first nucleic acid encoding
CC   streptavidin or its functional variant operatively linked to a promoter,
CC   and a cloning site for insertion of a second nucleic acid sequence
CC   encoding a polypeptide to be fused with streptavidin, interposed between
CC   the promoter and the first nucleic acid sequence. Alternatively, the
CC   vector construct comprises a first nucleic acid, operatively linked to a
CC   promoter, encoding a polypeptide to be fused with streptavidin, and a
CC   cloning site for insertion of a second nucleic acid encoding at least
CC   129 amino acids of streptavidin or its functional variant. The fusion
CC   proteins are useful for targeting tumour cells, particularly tumour cells
CC   associated with cancer, e.g. adenocarcinomas or hematological
CC   malignancies. The vector construct is useful for expressing of
CC   streptavidin fusion proteins. In particular, these are useful as tools
CC   for medical diagnostics and therapeutic purposes, e.g. for detecting the
CC   presence or absence of, or treating, a target site within a mammalian
CC   host.
XX
SQ   Sequence   431 AA;

  Query Match             79.9%;  Score 523.5;  DB 22;  Length 431;
  Best Local Similarity   82.9%;  Pred. No. 2e-40;
  Matches  102;  Conservative    8;  Mismatches   10;  Indels    3;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||||||||||||||||||:|||||||| |:|||||||| ||
Db     148 qvqlvqsgaevkkpgasvkvsckasgfnikdtymhwvrqapgqglqwmgridpangntks 207

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |  |||||||||||| :|||||||||||:|||||||:||      | :::||||||||||
Db     208 dlsfqgrvtitadtsintaymelsslrsddtavyycsrevl---tgtwsldywgqgtlvt 264

Qy     121 VSS 123
           |||
Db     265 vss 267
```

```
RESULT  10
AAR76681
ID   AAR76681 standard; Protein; 136 AA.
XX
AC   AAR76681;
XX
DT   17-JAN-1996  (first entry)
XX
DE   Human/murine chimeric antibody HEF-RVL-M21g(gamma)1.
XX
KW   Human; murine; chimeric antibody; HEF-RVL-M21g(gamma)1;
KW   medulloblastoma; brain tumour; treatment; diagnosis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1..19
FT                    /label= sig_peptide
FT   Peptide          20..50
FT                    /label= FR 1
FT   Peptide          51..55
FT                    /label= CDR 1
FT   Peptide          56..59
FT                    /label= FR 2
FT   Peptide          70..86
FT                    /label= CDR 2
FT   Peptide          87..118
FT                    /label= FR 3
FT   Peptide          119..126
FT                    /label= CDR 3
FT   Peptide          127..136
FT                    /label= FR 4
XX
PN   WO9514041-A1.
XX
PD   26-MAY-1995.
XX
PF   19-OCT-1994;   94WO-JP01763.
XX
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Ohtomo T,  Sato K,  Tsuchiya M;
XX
DR   WPI; 1995-200347/26.
DR   N-PSDB; AAQ94539.
XX
PT   Reconstituted antibody against human medullo:blastoma cells -
PT   contains high proportion of human antibody origin and has low
PT   antigenicity
XX
PS   Claim 26; Page 94; 120pp; Japanese.
XX
CC   AAQ94539 encodes AAR76681 the human/murine chimeric antibody HEF-
CC   RVL-M21g(gamma)1. The antibody is reactive with human medullo-
CC   blastoma (a brain tumour) cells. The chimeric antibody can be
CC   used in the diagnosis and treatment of this disease.
XX
SQ   Sequence   136 AA;

  Query Match             79.8%;  Score 523;  DB 16;  Length 136;
  Best Local Similarity   83.7%;  Pred. No. 6.2e-41;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||:|||||||||||||||||||||||| ||||||||||:| |||
Db      20 qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||||||| | :|||||||||||||| |:||   || |      |||||| ||
Db      80 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn-----qdywgqgttvt 133
```

```
Qy     121 VSS 123
           |||
Db     134 vss 136


RESULT  11
AAW04396
ID   AAW04396 standard; Protein; 136 AA.
XX
AC   AAW04396;
XX
DT   09-DEC-1996  (first entry)
XX
DE   Chimaeric human/murine MAb ONS-M21 fragment HEF-RVL-M21-g(gamma)1.
XX
KW   Murine; human; myeloblastoma; chimaera; monoclonal antibody;
KW   chimera; single stranded Fv region; low human antigenicity;
KW   diagnosis; treatment; cerebral tumour; reshaped.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= sig_peptide
FT   Peptide         20..136
FT                   /label= mat_peptide
FT   Region          50..54
FT                   /label= CDR_1
FT   Region          69..85
FT                   /label= CDR_2
FT   Region          118..125
FT                   /label= CDR_3
XX
PN   JP08169900-A.
XX
PD   02-JUL-1996.
XX
PF   18-NOV-1994;   94JP-0285057.
XX
PR   18-OCT-1994;   94JP-0252166.
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS ) CHUGAI PHARM CO LTD.
XX
DR   WPI; 1996-358509/36.
DR   N-PSDB; AAT38653.
XX
PT   Reshaped anti-human myeloblastoma cell human antibody - has low
PT   human antigenicity, and is therefore useful for diagnosis and
PT   treatment of cerebral tumours, e.g. myeloblastoma
XX
PS   Example 5; Pages 38-39; 45pp; Japanese.
XX
CC   The present sequence is a fragment of the chimaeric human/murine
CC   monoclonal antibody (MAb) ONS-M21. The MAb was prepd. by
CC   combining light and heavy variable region DNA, from a murine
CC   anti-human myeloblastoma cell MAb, with human light and heavy
CC   constant region sequences, respectively to produce chimaeric
CC   human/murine light and heavy chain DNA mols.. A recombinant vector
CC   for the expression of the heavy and light chain DNA mols. was
CC   prepd., and used to transform a host cell. The host cell was then
CC   cultured, and the expression prods. of the heavy and light chain
CC   DNA mols. sepd. and connected with a peptide linker to produce a
CC   single stranded Fv region. The reshaped Fv region has low human
CC   antigenicity, and is therefore expected to be useful as an agent
CC   for the diagnosis and treatment of cerebral tumours,
CC   e.g. myeloblastoma.
XX
SQ   Sequence   136 AA;

  Query Match             79.8%;  Score 523;  DB 17;  Length 136;
  Best Local Similarity   83.7%;  Pred. No. 6.2e-41;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||:|||||||||||||||||||||||||| ||||||||||:| |||
Db      20 qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||||||||| | :|||||||||||||| |:||   || |     ||||||| ||
Db      80 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn-----qdywgqgttvt 133

Qy     121 VSS 123
           |||
Db     134 vss 136


RESULT  12
AAR76682
ID   AAR76682 standard; Protein; 269 AA.
XX
AC   AAR76682;
XX
DT   18-JAN-1996  (first entry)
XX
DE   Human ONS-M21 antibody Fv fragment.
XX
KW   Plasmid pSCFVT7-hM21; human; ONS-M21 antibody; chimeric protein;
KW   medulloblastoma; brain tumour; treatment; diagnosis; Fv fragment.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= sig_peptide
FT   Region          23..139
FT                   /note= "heavy variable region"
FT   Region          140..154
FT                   /note= "linker"
FT   Region          155..269
FT                   /note= "light variable region"
FT   Region          262..269
FT                   /note= "FLAG"
XX
PN   WO9514041-A1.
XX
PD   26-MAY-1995.
XX
PF   19-OCT-1994;   94WO-JP01763.
XX
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Ohtomo T,  Sato K,  Tsuchiya M;
XX
DR   WPI; 1995-200347/26.
DR   N-PSDB; AAQ94548.
XX
PT   Reconstituted antibody against human medullo:blastoma cells -
PT   contains high proportion of human antibody origin and has low
PT   antigenicity
XX
PS   Claim 35; Pages 98-99; 120pp; Japanese.
XX
CC   AAQ94548 is the plasmid pSCFVT7-hM21, which encodes AAR76682 the
CC   human antibody ONS-M21 Fv fragment. The plasmid was used in the
CC   construction of an expression vector, contg. cDNA encoding a
CC   human/murine chimeric antibody, reactive with human medullo-
CC   blastoma (a brain tumour) cells. The chimeric antibody can be
CC   used in the diagnosis and treatment of this disease.
XX
SQ   Sequence   269 AA;
```

```
  Query Match             79.8%;  Score 523;  DB 16;  Length 269;
  Best Local Similarity   83.7%;  Pred. No. 1.3e-40;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||:|||||||||||||||||||||||||| |||||||||||:| |||
Db      23 qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 82

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||||||| | :|||||||||||||| |:||   || |      ||||||| ||
Db      83 dpkfqgrvtitadestntaymelsslrsedtafyfca-sayyvn-----qdywgqgttvt 136

Qy     121 VSS 123
           |||
Db     137 vss 139


RESULT  13
AAW04397
ID   AAW04397 standard; Protein; 269 AA.
XX
AC   AAW04397;
XX
DT   09-DEC-1996  (first entry)
XX
DE   Chimaeric human/murine MAb ONS-M21 scFv fragment.
XX
KW   Murine; human; myeloblastoma; chimaera; monoclonal antibody;
KW   chimera; single stranded Fv region; low human antigenicity;
KW   diagnosis; treatment; cerebral tumour; reshaped.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= sig_peptide
FT   Region          23..139
FT                   /note= "heavy variable region"
FT   Peptide         140..154
FT                   /label= linker
FT   Region          155..261
FT                   /note= "light variable region"
FT   Peptide         262..269
FT                   /label= FLAG
XX
PN   JP08169900-A.
XX
PD   02-JUL-1996.
XX
PF   18-NOV-1994;   94JP-0285057.
XX
PR   18-OCT-1994;   94JP-0252166.
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS ) CHUGAI PHARM CO LTD.
XX
DR   WPI; 1996-358509/36.
DR   N-PSDB; AAT38662.
XX
PT   Reshaped anti-human myeloblastoma cell human antibody - has low
PT   human antigenicity, and is therefore useful for diagnosis and
PT   treatment of cerebral tumours, e.g. myeloblastoma
XX
PS   Example 6; Pages 40-41; 45pp; Japanese.
XX
CC   The present sequence is a scFv fragment from the chimaeric
CC   human/murine monoclonal antibody (MAb) ONS-M21. The MAb was
CC   prepd. by combining light and heavy variable region DNA, from a
CC   murine anti-human myeloblastoma cell MAb, with human light and
CC   heavy constant region sequences, respectively to produce chimaeric
CC   human/murine light and heavy chain DNA mols.. A recombinant vector
CC   for the expression of the heavy and light chain DNA mols. was
CC   prepd., and used to transform a host cell. The host cell was then
CC   cultured, and the expression prods. of the heavy and light chain
CC   DNA mols. sepd. and connected with a peptide linker to produce a
CC   single stranded Fv region. The reshaped Fv region has low human
CC   antigenicity, and is therefore expected to be useful as an agent
CC   for the diagnosis and treatment of cerebral tumours,
CC   e.g. myeloblastoma.
XX
SQ   Sequence   269 AA;


  Query Match             79.8%;  Score 523;  DB 17;  Length 269;
  Best Local Similarity   83.7%;  Pred. No. 1.3e-40;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Db      23 qvqlvqsgaevkkpgssvkvsckasgfnikdtyihwvrqapgqglewmgridpadgntky 82

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Qy     121 VSS 123
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Db     137 vss 139


RESULT  14
AAR81325
ID   AAR81325 standard; Protein; 119 AA.
XX
AC   AAR81325;
XX
DT   02-APR-1996  (first entry)
XX
DE   Humanized VLA-4 antibody 21.6 heavy chain variable region, Hc.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Claim 13; Page 70; 105pp; English.
XX
CC   The sequence encodes the mouse antibody 21.6 heavy chain variable
CC   region, Hc, directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions
CC   are linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
```

```
CC   21.6 Ig L chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   for inhibiting adhesion of a leukocyte to an endothelial cell and
CC   for treating inflammatory diseases such as multiple sclerosis.  They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   119 AA;


  Query Match             78.6%;  Score 515;  DB 16;  Length 119;
  Best Local Similarity   82.9%;  Pred. No. 2.9e-40;
  Matches  102;  Conservative    5;  Mismatches   12;  Indels    4;  Gaps    1;

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Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Qy     121 VSS 123
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Db     117 vss 119


RESULT  15
AAW22426
ID   AAW22426 standard; Protein; 119 AA.
XX
AC   AAW22426;
XX
DT   09-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VH Hc.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1..30
FT                   /label= FR1
FT                   /note= "21/28'CL framework region 1"
FT   Misc-difference 27..30
FT                   /note= "21/28'CL residues 27-30 are replaced by
FT                         those of MAb 21.6, involved in antigen
FT                         binding"
FT   Region          31..35
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          36..49
FT                   /label= FR2
FT                   /note= "21/28'CL framework region 2"
FT   Region          50..66
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          67..98
FT                   /label= FR3
FT                   /note= "21/28'CL framework region 3"
FT   Misc-difference 72
FT                   /note= "21/28'CL Arg-72 is substd. by Ala of mouse
FT                         21.6 VL, important in supporting the CDR2
FT                         loop"
FT   Region          99..112
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Misc-difference 102
FT                   /note= "21/28'CL Tyr-102 is substd. by Phe of human
FT                         VCAM-1"
FT   Region          113..123
FT                   /label= FR4
FT                   /note= "21/28'CL framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones ST,  Leger OJ,  Saldanha J,  Yednock TA;
XX
DR   WPI; 1997-297879/27.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 5; Fig 7; 107pp; English.
XX
CC   This polypeptide, designated Hc, comprises the heavy chain variable
CC   region (VH) of a humanised alpha-4 integrin antibody 21.6.  It is
CC   composed of complementarity determining regions (CDRs) from the VH
CC   region (see AAW22410) of mouse alpha-4 integrin monoclonal antibody
CC   21.6 and a modified human 21/28'CL framework.  It contains an
CC   additional amino acid substitution (Tyr102Phe) in comparison to
CC   claimed humanised 21.6 VH version Ha (see AAW22412).  Humanised
CC   21.6 VH and VL regions are used to produce claimed humanised 21.6
CC   antibodies useful in the manufacture of a medicament for treating
CC   asthma, atherosclerosis, AIDS, dementia, diabetes, inflammatory
CC   bowel disease, rheumatoid arthritis, transplant rejection, graft
CC   versus host disease, tumour metastasis, nephritis, atopic
CC   dermatitis, psoriasis, myocardial ischaemia, and acute leukocyte
CC   mediated lung injury.  The humanised antibodies have a half-life
CC   in the human circulation essentially equivalent to that of
CC   naturally occurring human antibodies.
XX
SQ   Sequence   119 AA;


  Query Match             78.6%;  Score 515;  DB 18;  Length 119;
  Best Local Similarity   82.9%;  Pred. No. 2.9e-40;
  Matches  102;  Conservative    5;  Mismatches   12;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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Db       1 qvqlvqsgaevkkpgasvkvsckasgfniksyamhwvrqapgqrlewmgwinagngntky 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
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Qy     121 VSS 123
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:23:04 ; Search time 32.41 Seconds
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85.403 Million cell updates/sec

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Perfect score: 655
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Scoring table: BLOSUM62
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Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	655	100.0	123	2	US-08-561-521-11	Sequence 11, Appl
2	655	100.0	123	5	PCT-US95-01219-11	Sequence 11, Appl
3	655	100.0	142	2	US-08-561-521-17	Sequence 17, Appl
4	655	100.0	142	5	PCT-US95-01219-17	Sequence 17, Appl
5	552	84.3	123	2	US-08-561-521-9	Sequence 9, Appli
6	552	84.3	123	5	PCT-US95-01219-9	Sequence 9, Appli
7	544	83.1	140	2	US-08-561-521-4	Sequence 4, Appli
8	544	83.1	140	5	PCT-US95-01219-4	Sequence 4, Appli
9	523	79.8	117	4	US-08-646-265A-132	Sequence 132, App
10	523	79.8	136	4	US-08-646-265A-99	Sequence 99, Appl
11	523	79.8	269	4	US-08-646-265A-109	Sequence 109, App
12	515	78.6	119	2	US-08-561-521-13	Sequence 13, Appl
13	515	78.6	119	5	PCT-US95-01219-13	Sequence 13, Appl
14	512	78.2	119	2	US-08-561-521-12	Sequence 12, Appl
15	512	78.2	119	5	PCT-US95-01219-12	Sequence 12, Appl
16	505	77.1	125	2	US-08-561-521-44	Sequence 44, Appl
17	505	77.1	125	5	PCT-US95-01219-44	Sequence 44, Appl
18	495	75.6	119	2	US-08-561-521-10	Sequence 10, Appl
19	495	75.6	119	5	PCT-US95-01219-10	Sequence 10, Appl
20	492	75.1	117	2	US-08-290-592E-17	Sequence 17, Appl
21	492	75.1	117	5	PCT-US95-10053-14	Sequence 14, Appl
22	492	75.1	117	5	PCT-US96-09448-17	Sequence 17, Appl
23	491.5	75.0	118	2	US-08-232-081B-8	Sequence 8, Appli
24	489.5	74.7	120	4	US-09-025-769B-36	Sequence 36, Appl
25	489.5	74.7	120	4	US-09-025-769B-59	Sequence 59, Appl
26	486	74.2	140	3	US-08-836-561-63	Sequence 63, Appl
27	484.5	74.0	135	1	US-08-137-117D-112	Sequence 112, App
28	484.5	74.0	135	2	US-08-436-717-112	Sequence 112, App
29	484.5	74.0	139	1	US-08-253-877C-19	Sequence 19, Appl
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33	481	73.4	121	3	US-08-964-690-23	Sequence 23, Appl
34	474	72.4	140	3	US-08-836-561-74	Sequence 74, Appl
35	473	72.2	123	1	US-08-482-882-53	Sequence 53, Appl
36	473	72.2	123	2	US-08-483-389-53	Sequence 53, Appl
37	473	72.2	123	2	US-08-487-113D-53	Sequence 53, Appl
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39	473	72.2	123	2	US-08-483-932-53	Sequence 53, Appl
40	473	72.2	123	2	US-08-720-420A-53	Sequence 53, Appl
41	473	72.2	123	3	US-08-714-017-53	Sequence 53, Appl
42	473	72.2	123	3	US-08-475-680-53	Sequence 86, Appl
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ALIGNMENTS

RESULT 1
US-08-561-521-11
; Sequence 11, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 123 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-11

Query Match 100.0%; Score 655; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;

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Db       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

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Qy     121 VSS 123
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Db     121 VSS 123


RESULT   2
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; Sequence 11, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-11


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Qy     121 VSS 123
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RESULT   3
US-08-561-521-17
; Sequence 17, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  142 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-17


  Query Match             100.0%;  Score 655;  DB 2;  Length 142;
  Best Local Similarity   100.0%;  Pred. No. 2e-58;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      80 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 139

Qy     121 VSS 123
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Db     140 VSS 142


RESULT   4
PCT-US95-01219-17
; Sequence 17, Application PC/TUS9501219
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;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  142 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-17


  Query Match             100.0%;  Score 655;  DB 5;  Length 142;
  Best Local Similarity   100.0%;  Pred. No. 2e-58;
  Matches  123;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      80 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 139

Qy     121 VSS 123
           |||
Db     140 VSS 142


RESULT   5
US-08-561-521-9
; Sequence 9, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-9


  Query Match             84.3%;  Score 552;  DB 2;  Length 123;
  Best Local Similarity   82.9%;  Pred. No. 3.3e-48;
  Matches  102;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||||| |||||||:|| |||||||||||| |:| | | |||:||||||||||||||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||| |||||||::|||::|||| |||||||:|||||||||||||||||||| ||
Db      61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120

Qy     121 VSS 123
           |||
Db     121 VSS 123


RESULT   6
PCT-US95-01219-9
; Sequence 9, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/01219
;       FILING DATE:  25-JAN-1995
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/186,269
;       FILING DATE:  25-JAN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William L.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  15270-14
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-543-9600
;       TELEFAX:  415-543-5043
;   INFORMATION FOR SEQ ID NO:  9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  123 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US95-01219-9


  Query Match             84.3%;  Score 552;  DB 5;  Length 123;
  Best Local Similarity   82.9%;  Pred. No. 3.3e-48;
  Matches  102;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||||| |||||||:|| |||||||||||| |:| | | |||:||||||||||||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||| ||||||::|||::|||| |||||||:||||||||||||||||||||| ||
Db      61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120

Qy     121 VSS 123
           |||
Db     121 VSS 123


RESULT   7
US-08-561-521-4
; Sequence 4, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  140 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-4


  Query Match             83.1%;  Score 544;  DB 2;  Length 140;
  Best Local Similarity   82.6%;  Pred. No. 2.4e-47;
  Matches  100;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||||| |||||||:|| |||||||||||| |:| | | |||:||||||||||||
Db      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||| ||||||::|||::|||| |||||||:||||||||||||||||||||| ||
Db      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139

Qy     121 V 121
           |
Db     140 V 140


RESULT   8
PCT-US95-01219-4
; Sequence 4, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  140 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-4


  Query Match             83.1%;  Score 544;  DB 5;  Length 140;
  Best Local Similarity   82.6%;  Pred. No. 2.4e-47;
  Matches  100;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: ||||||:|| |||||||||||| |:| | | |||:||||||||||||
Db      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||: ||||||||::|||::|||| |||||||:||||||||||||||||||| ||
Db      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139

Qy     121 V 121
           |
Db     140 V 140


RESULT   9
US-08-646-265A-132
; Sequence 132, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  132:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-132


  Query Match             79.8%;  Score 523;  DB 4;  Length 117;
  Best Local Similarity   83.7%;  Pred. No. 2.4e-45;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||:|||||||||||||||||||||||||| ||||||||||:| |||
Db       1 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||||||||| | :|||||||||||||||| |:||   || |      ||||||| ||
Db      61 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 114

Qy     121 VSS 123
           |||
Db     115 VSS 117


RESULT  10
US-08-646-265A-99
; Sequence 99, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  99:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  136 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-99


  Query Match             79.8%;  Score 523;  DB 4;  Length 136;
  Best Local Similarity   83.7%;  Pred. No. 2.9e-45;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
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          |||||||||||||||:||||||||||||||||||||||||| ||||||||||:| |||
Db      20 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |||||||||||||| | :|||||||||||||||| |:||   || |      ||||||| ||
Db      80 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 133

Qy     121 VSS 123
          |||
Db     134 VSS 136


RESULT 11
US-08-646-265A-109
; Sequence 109, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  109:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  269 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-109


  Query Match             79.8%;  Score 523;  DB 4;  Length 269;
  Best Local Similarity   83.7%;  Pred. No. 6.5e-45;
  Matches  103;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||||||||||||||:|||||||||||||||||||||||| ||||||||||:| |||
Db      23 QVQLVQSGAEVKKPGSSVKVSCKASGFNIKDTYIHWVRQAPGQGLEWMGRIDPADGNTKY 82

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |||||||||||||| | :|||||||||||||||| |:||   || |      ||||||| ||
Db      83 DPKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-SAYYVN-----QDYWGQGTTVT 136

Qy     121 VSS 123
          |||
Db     137 VSS 139


RESULT 12
US-08-561-521-13
; Sequence 13, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-13


  Query Match             78.6%;  Score 515;  DB 2;  Length 119;
  Best Local Similarity   82.9%;  Pred. No. 1.6e-44;
  Matches  102;  Conservative    5;  Mismatches   12;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||||||||||||||||||||||||||||    :|||||||||||||| |:  || |||
Db       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
            |||||||||||||||||||||||||||||||||||| ||:|:      :|||||||||
Db      61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYFGS----GSNYWGQGTLVT 116

Qy     121 VSS 123
          |||
Db     117 VSS 119


RESULT 13
PCT-US95-01219-13
```

```
; Sequence 13, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-13


  Query Match             78.6%;  Score 515;  DB 5;  Length 119;
  Best Local Similarity   82.9%;  Pred. No. 1.6e-44;
  Matches  102;  Conservative    5;  Mismatches   12;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||||||   :|||||||||||||| |:  || |||
Db       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQRLEWMGWINAGNGNTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
             ||||||||||||||||||||||||||||||||| ||:|:      :|||||||||
Db      61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYFGS----GSNYWGQGTLVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119


RESULT  14
US-08-561-521-12
; Sequence 12, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-12


  Query Match             78.2%;  Score 512;  DB 2;  Length 119;
  Best Local Similarity   82.9%;  Pred. No. 3.1e-44;
  Matches  102;  Conservative    4;  Mismatches   13;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||||||   :|||||||| ||||| |:  || |||
Db       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQGLEWMGWINAGNGNTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
             |||||||||||||||||||||||||||||||| ||||:      :|||||||||
Db      61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYYGS----GSNYWGQGTLVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119


RESULT  15
PCT-US95-01219-12
; Sequence 12, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
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;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-12


  Query Match             78.2%;  Score 512;  DB 5;  Length 119;
  Best Local Similarity   82.9%;  Pred. No. 3.1e-44;
  Matches  102;  Conservative    4;  Mismatches   13;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||||||||||||||||||   :||||||||| ||||| |:  || |||
Db       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKSYAMHWVRQAPGQGLEWMGWINAGNGNTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
             ||||||||||||||||||||||||||||||||||| ||||:      :|||||||||
Db      61 SQKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARGGYYGS----GSNYWGQGTLVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119


Search completed: May  7, 2002, 12:23:04
Job time: 175 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:23:47 ; Search time 37.68 Seconds
(without alignments)
248.659 Million cell updates/sec

Title: US-09-155-739-11
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....NYGVYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	488.5	74.6	178	2	S29594	Ig gamma chain (WM
2	477	72.8	120	2	S03471	Ig heavy chain V-D
3	473.5	72.3	118	2	S36265	Ig heavy chain V r
4	468	71.5	123	2	D33548	Ig heavy chain V-1
5	467	71.3	142	2	A32483	Ig heavy chain V r
6	465	71.0	117	2	S17586	Ig heavy chain V r
7	459.5	70.2	122	2	S06823	Ig heavy chain V r
8	456.5	69.7	132	2	PH0954	Ig heavy chain V r
9	455	69.5	116	2	S24289	Ig gamma chain V r
10	455	69.5	221	2	S49220	Ig gamma-1 chain -
11	450	68.7	129	2	S46393	Ig heavy chain V r
12	449	68.5	115	2	S03482	Ig heavy chain V-D
13	447.5	68.3	135	2	S49530	anti-Sm antibody V
14	447	68.2	120	2	S03484	Ig heavy chain V-D
15	446.5	68.2	136	2	PH0960	Ig heavy chain V r
16	444	67.8	136	2	S04576	Ig heavy chain pre
17	443	67.6	119	2	PH0961	Ig heavy chain V r
18	441.5	67.4	268	2	A56446	Ig heavy chain V r
19	439.5	67.1	104	2	PH1665	Ig heavy chain V r
20	439.5	67.1	114	4	A47271	nitrophenyl phosph
21	439	67.0	133	2	C33548	Ig heavy chain V-1
22	439	67.0	627	2	S14683	Ig mu chain precur
23	438.5	66.9	114	2	PH1667	Ig heavy chain V r
24	438.5	66.9	118	2	PH1666	Ig heavy chain V r
25	437.5	66.8	137	2	S52445	Ig heavy chain V r
26	436.5	66.6	120	2	S31999	Ig heavy chain V r
27	435.5	66.5	120	2	PH0962	Ig heavy chain V r
28	435.5	66.5	128	2	PH0952	Ig heavy chain V-1
29	433.5	66.2	126	2	B33548	Ig heavy chain V r
30	433	66.1	127	2	PH0955	Ig heavy chain V r
31	433	66.1	135	2	PH0953	Ig heavy chain V r
32	431	65.8	126	2	I44151	Ig heavy chain V r
33	429.5	65.6	108	2	PH1012	Ig heavy chain V r
34	429	65.5	125	2	PH0957	Ig heavy chain pre
35	427.5	65.3	143	1	E1HUND	Ig heavy chain V r
36	427	65.2	125	2	S68170	Ig heavy chain V-1
37	427	65.2	129	2	A33548	Ig heavy chain V r
38	426	65.0	127	2	S34014	Ig heavy chain V r
39	425	64.9	129	2	S36260	Ig heavy chain V r
40	424.5	64.8	147	2	PH1561	Ig heavy chain V r
41	424.5	64.8	171	2	S23623	Ig gamma chain - m
42	421	64.3	246	2	S38950	Ig gamma-2a chain
43	421	64.3	446	2	S40295	Ig heavy chain V r
44	420.5	64.2	122	2	PH1426	Ig heavy chain V r
45	420	64.1	121	2	S20783	

ALIGNMENTS

RESULT 1
S29594
Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S29594
R;Seymour, R.
submitted to the EMBL Data Library, February 1991
A;Reference number: S29593
A;Accession: S29594
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <SEY>
A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C;Keywords: immunoglobulin

Query Match 74.6%; Score 488.5; DB 2; Length 178;
Best Local Similarity 75.6%; Pred. No. 9e-37;
Matches 93; Conservative 11; Mismatches 14; Indels 5; Gaps 2;

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Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||||| |||||||:|| |||||||||||:|||:| | | |||:|||||||||||:|
Db      14 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEWIGRIDPANGYTEY 73

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||| ||||||| :|||::|||| |||||||||      ||| | |||||||| ||
Db      74 DPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTG----GNY-AYGMDYWGQGTSVT 128

Qy     121 VSS 123
           |||
Db     129 VSS 131
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RESULT 2
S03471
Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-hypervariable regions.
A;Reference number: S03471; MUID:84057768
A;Accession: S03471
A;Molecule type: mRNA
A;Residues: 7-120 <ROC1>
A;Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug J. Immunol. 129, 2554-2558, 1982

A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.8%; Score 477; DB 2; Length 120;
Best Local Similarity 75.6%; Pred. No. 6.3e-36;
Matches 93; Conservative 11; Mismatches 15; Indels 4; Gaps 1;

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Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: |||||||:|| ||||||||||:|||:| | | |||:|||||||| |||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||: |||||||::|||::|||| |||||||||||    |     ||||||||| ||
Db      61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR----GWLRRDAMDYWGQGTSVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119
```

RESULT 3
S36265
Ig heavy chain V region (clone alpha-MUC1-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36265
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448
A;Accession: S36265
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-118 <GRI>
A;Cross-references: EMBL:Z18846; NID:g33121; PIDN:CAA79298.1; PID:g939900
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.3%; Score 473.5; DB 2; Length 118;
Best Local Similarity 76.2%; Pred. No. 1.3e-35;
Matches 96; Conservative 6; Mismatches 13; Indels 11; Gaps 2;

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Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||:     |:|||||||| ||||| |:| :| | |
Db       1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE---GYYGNYGVYAMDYWGQGT 117
           |||||||| |||||||||||||||||||||||:   ||        :|||||||
Db      61 AQKFQGRVTITRDTSASTAYMELSSLRSEDTAVYYCARDFLSGY--------LDYWGQGT 112

Qy     118 LVTVSS 123
           ||||||
Db     113 LVTVSS 118
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RESULT 4
D33548
Ig heavy chain V-1 region (WIL2) - human
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change 16-Aug-1996
C;Accession: D33548
R;Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
Proc. Natl. Acad. Sci. U.S.A. 86, 5913-5917, 1989
A;Title: Developmentally restricted immunoglobulin heavy chain variable region gene expr
A;Reference number: A33548; MUID:89345575
A;Accession: D33548
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A;Molecule type: mRNA
A;Residues: 1-123 <KIP>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.5%; Score 468; DB 2; Length 123;
Best Local Similarity 74.8%; Pred. No. 4.1e-35;
Matches 92; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

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Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||:|||:     |:||||||||| ||||| |:| :| | |
Db       1 QVQLVQSGAEVKKPGASVKVSCEASGYTFTGHYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
             |||||||| ||| :|||||| |||:|||||||||  | |     |  ||||||||||
Db      61 AEKFQGRVTITRDTSINTAYMELSRLRSDDTAVYYCARASYCGYDCYYFFDYWGQGTLVT 120

Qy     121 VSS 123
           |||
Db     121 VSS 123
```

RESULT 5
A32483
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C;Accession: A32483
R;Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A;Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells
A;Reference number: A32483; MUID:89273586
A;Accession: A32483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-142 <LAR>
A;Cross-references: GB:M26463
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-108/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 467; DB 2; Length 142;
Best Local Similarity 73.2%; Pred. No. 5.9e-35;
Matches 93; Conservative 8; Mismatches 22; Indels 4; Gaps 1;

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Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||:   : |:|||||||| ||||| |:|:   | |
Db      11 QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYYMHWVRQAPGQGLEWMGIINPSGNSTNY 70

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE----GYYGNYGVYAMDYWGQG 116
           |||||||:| ||| || |||||||||||||||||||||      :|   :  |||||||
Db      71 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAREKLATTIFGVLIITGMDYWGQG 130

Qy     117 TLVTVSS 123
           |||||||
Db     131 TLVTVSS 137
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RESULT 6
S17586
Ig heavy chain V region (E8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S17586
R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochr

forms.
A;Reference number: S17586; MUID:92015240
A;Accession: S17586
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <MYL>
A;Cross-references: EMBL:X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 71.0%; Score 465; DB 2; Length 117;
Best Local Similarity 72.6%; Pred. No. 7.3e-35;
Matches 90; Conservative 15; Mismatches 11; Indels 8; Gaps 3;

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Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||||| |||||||:|| |||||||||||:|||:| | : |||:|||||:| |||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEKGLEWIGRIDPASGNTKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY-YGNYGVYAMDYWGQGTLV 119
           ||||| : |||||||::|||::|||| |||||||||| || |||:     ||||||| :
Db      61 DPKFQDKATITADTSSNTAYLQLSSLTSEDTAVYYCA--GYDYGNF-----DYWGQGTTL 113

Qy     120 TVSS 123
           ||||
Db     114 TVSS 117
```

RESULT 7
S06823
Ig heavy chain V region (clone IIc) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06823
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531
A;Accession: S06823
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-122 <MIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 70.2%; Score 459.5; DB 2; Length 122;
Best Local Similarity 73.4%; Pred. No. 2.4e-34;
Matches 91; Conservative 13; Mismatches 17; Indels 3; Gaps 3;

```
Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIH-WVRQAPGQRLEWMGRIDPANGYTK 59
           :||| ||||| |||||||:|| |||||||||||:| ||:| | | |||:||||||||| ||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHEWVKQRPEQGLEWIGRIDPANGNTK 60

Qy      60 YDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLV 119
           |||||||: |||||||::|||::|||| |||||||||| |:       :|||||| |
Db      61 YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR-GWL-RRDAMGVDYWGQGTSV 118

Qy     120 TVSS 123
           ||||
Db     119 TVSS 122
```

RESULT 8
PH0954
Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0954
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0954
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-132 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-120/Region: complementarity-determining 3

Query Match 69.7%; Score 456.5; DB 2; Length 132;
Best Local Similarity 72.0%; Pred. No. 4.8e-34;
Matches 95; Conservative 1; Mismatches 27; Indels 9; Gaps 1;

```
Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||:||||||||||          | |||||||| ||||| | |  |   |
Db       1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR---------EGYYGNYGVYAMD 111
           |||||||||| | |||||||||||||||||||||          ||| ||  | ||
Db      61 AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARPHASIDDFWSGYYPNYYYYGMD 120

Qy     112 YWGQGTLVTVSS 123
           ||||| |||||
Db     121 VWGQGTTVTVSS 132
```

RESULT 9
S24289
Ig gamma chain V region (JS34/32) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
R;Moncharmont, B.
submitted to the EMBL Data Library, September 1991
A;Description: Cloning and sequencing of the cDNA coding for the variable regions of
A;Reference number: S24287
A;Accession: S24289
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MON>
A;Cross-references: EMBL:X62705; NID:g51690; PIDN:CAA44584.1; PID:g1333963
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>

Query Match 69.5%; Score 455; DB 2; Length 116;
Best Local Similarity 71.5%; Pred. No. 5.7e-34;
Matches 88; Conservative 13; Mismatches 14; Indels 8; Gaps 2;

```
Qy       2 VQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYD 61
           ||| :||||: |||||||:|| || |||:|||:||||| | | |||:|||||||| | :|
Db       1 VQLQESGAELVKPGASVKLSCTASVFNIQDTYMHWVRQRPKQGLEWIGRIDPANGNTHFD 60

Qy      62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLVT 120
           |||||: |||||||::|||::|||| ||||||||||  |||          ||||||| :|
Db      61 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARWAGYY-------FDYWGQGTTLT 113

Qy     121 VSS 123
           |||
Db     114 VSS 116
```

RESULT 10
S49220

Ig gamma-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C;Accession: S49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a
A;Reference number: S49220
A;Accession: S49220
A;Molecule type: mRNA
A;Residues: 1-221 <KIP>
A;Cross-references: EMBL:Z37502; NID:g541778; PIDN:CAA85732.1; PID:g541779
A;Experimental source: strain Balb/c
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-120/Domain: V region #status predicted <VRG>
F;121-221/Domain: C region #status predicted <CRG>
F;139-203/Domain: immunoglobulin homology <IMM>

Query Match 69.5%; Score 455; DB 2; Length 221;
Best Local Similarity 70.7%; Pred. No. 1.1e-33;
Matches 87; Conservative 12; Mismatches 20; Indels 4; Gaps 1;

```
Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          ||:|::|||| | |||||:|| |||||||||:|||:| | | |||:||||||||  ||
Db      1 QVKLLESGAELVKSGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGEIKY 60

Qy     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          ||||||  |||||||  :|||::|||| |||||||||  | |    ||     ||||||  :|
Db     61 DPKFQGTATITADTSTNTAYLQLSSLTSEDTAVYYCVRRG----YGSSQEPYWGQGTTLT 116

Qy    121 VSS 123
          |||
Db    117 VSS 119
```

RESULT 11
S46393
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46393
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092
A;Accession: S46393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <FIG>
A;Cross-references: EMBL:Z31680; NID:g509786; PIDN:CAA83485.1; PID:g1335146
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.7%; Score 450; DB 2; Length 129;
Best Local Similarity 70.5%; Pred. No. 1.8e-33;
Matches 91; Conservative 10; Mismatches 22; Indels 6; Gaps 2;

```
Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||||||||||||||||||||||||:     |:|||||||| ||||| |:| :| | |
Db      1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREG--YYGNYGVYA----MDYWG 114
          |||| ||:| ||| |||||||| |||:|||||||||:    || : | |:    || ||
Db     61 AQKFQGWVTMTRDTSISTAYMELSRLRSDDTAVYYCARDSAYYYDSSGYYSANYYMDVWG 120

Qy    115 QGTLVTVSS 123
          :|| |||||
Db    121 KGTTVTVSS 129
```

RESULT 12
S03482
Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03482; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
hypervariable regions.
A;Reference number: S03471; MUID:84057768
A;Accession: S03482
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-115 <ROC1>
A;Cross-references: EMBL:X03219
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 68.5%; Score 449; DB 2; Length 115;
Best Local Similarity 70.2%; Pred. No. 1.9e-33;
Matches 85; Conservative 12; Mismatches 18; Indels 6; Gaps 1;

```
Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
            :||| ||||||: |||||||:|| |||||||||:|||:| | | |||:|||||| | |||
Db      1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPAKGNTKY 60

Qy     61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
          |||||||: ||| |||::|||:: ||| ||||||||||||     |       |||||||  :|
Db     61 DPKFQGKATITTDTSSNTAYLQFSSLTSEDTAVYYCARGTTVGR------DYWGQGTTLT 114

Qy    121 V 121
          |
Db    115 V 115
```

RESULT 13
S49530
anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b) - human
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C;Accession: S49530
R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodies.
A;Reference number: S48797
A;Accession: S49530
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <MAH>
A;Cross-references: EMBL:Z46348; NID:g560839; PIDN:CAA86467.1; PID:g560840
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 68.3%; Score 447.5; DB 2; Length 135;
Best Local Similarity 72.8%; Pred. No. 3.1e-33;
Matches 91; Conservative 7; Mismatches 16; Indels 11; Gaps 2;

```
Qy      1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
          |||||||||||||||||||||||||:     |:|||||||| ||||| |:| :| | |
```

```
Db      20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYC--AREGYYGNYGVYAMDYWGQGTL 118
           |||||||:| ||| |||||||| |||:|||||||  || ||         :|||||||
Db      80 AQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCARARTGY---------NYWGQGTL 130

Qy     119 VTVSS 123
           |||||
Db     131 VTVSS 135


RESULT  14
S03484
Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03484; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
hypervariable regions.
A;Reference number: S03471; MUID:84057768
A;Accession: S03484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-120 <ROC1>
A;Cross-references: EMBL:X07144
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match             68.2%;  Score 447;  DB 2;  Length 120;
  Best Local Similarity   71.5%;  Pred. No. 3e-33;
  Matches   88;  Conservative   11;  Mismatches   20;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: ||||||:|| ||||||||||:|||:| | | |||:||||||| :||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANXNSKY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
             |||||  ||||||||:| ||::|||| | ||||||| |    | :   |||||||||| ||
Db      61 GPKFQGXATITADTSSSAAYLQLSSLTSGDTAVYYCTR----GWFRRDAMDYWGQGTSVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119


RESULT  15
PH0960
Ig heavy chain V region (G6+ T-L30) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
C;Accession: PH0960
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880
A;Accession: PH0960
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-136 <MAR>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-30/Region: framework 1
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;36-50/Region: framework 2
F;51-67/Region: complementarity-determining 2
F;68-98/Region: framework 3
F;99-124/Region: complementarity-determining 3


  Query Match             68.2%;  Score 446.5;  DB 2;  Length 136;
  Best Local Similarity   69.1%;  Pred. No. 3.8e-33;
  Matches   94;  Conservative    1;  Mismatches   28;  Indels   13;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||||||:|||||||||||          | |||||||| ||||| | |  |   |
Db       1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIIPIFGTANY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-------------EGYYGNYGV 107
             |||||||||| | ||||||||||||||||||||||||                |||   |
Db      61 AQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCARGRTRVSVSTLYDSSGYYDFSGY 120

Qy     108 YAMDYWGQGTLVTVSS 123
           | || ||||| |||||
Db     121 YGMDVWGQGTTVTVSS 136


Search completed: May  7, 2002, 12:23:48
Job time: 199 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:32:34 ; Search time 21.92 Seconds
(without alignments)
205.738 Million cell updates/sec

Title: US-09-155-739-11
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....NYGVYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	427.5	65.3	147	1	HV1C_HUMAN	P01744 homo sapien
2	409	62.4	120	1	HV03_MOUSE	P01747 mus musculu
3	408.5	62.4	139	1	HV07_MOUSE	P01751 mus musculu
4	405	61.8	117	1	HV1B_HUMAN	P01743 homo sapien
5	399	60.9	140	1	HV02_MOUSE	P01746 mus musculu
6	396	60.5	117	1	HV1G_HUMAN	P23083 homo sapien
7	390	59.5	117	1	HV1A_HUMAN	P01742 homo sapien
8	378	57.7	117	1	HV13_MOUSE	P01757 mus musculu
9	375.5	57.3	118	1	HV51_MOUSE	P06330 mus musculu
10	373	56.9	117	1	HV12_MOUSE	P01756 mus musculu
11	371.5	56.7	137	1	HV11_MOUSE	P01755 mus musculu
12	369	56.3	138	1	HV48_MOUSE	P03980 mus musculu
13	364.5	55.6	120	1	HV50_MOUSE	P06329 mus musculu
14	360	55.0	121	1	HV01_MOUSE	P01745 mus musculu
15	360	55.0	136	1	HV15_MOUSE	P01759 mus musculu
16	355	54.2	125	1	HV1F_HUMAN	P06326 homo sapien
17	349.5	53.4	120	1	HV1H_HUMAN	P80421 homo sapien
18	349	53.3	117	1	HV09_MOUSE	P01753 mus musculu
19	344.5	52.6	114	1	HV00_MOUSE	P01741 mus musculu
20	338	51.6	117	1	HV04_MOUSE	P01748 mus musculu
21	336	51.3	117	1	HV06_MOUSE	P01750 mus musculu
22	333.5	50.9	136	1	HV16_MOUSE	P01783 mus musculu
23	333	50.8	117	1	HV10_MOUSE	P01754 mus musculu
24	330.5	50.5	124	1	HV1E_HUMAN	P01761 homo sapien
25	329	50.2	117	1	HV14_MOUSE	P01758 mus musculu
26	329	50.2	117	1	HV49_MOUSE	P06328 mus musculu
27	326	49.8	117	1	HV52_MOUSE	P06327 mus musculu
28	326	49.8	123	1	HV24_MOUSE	P01793 mus musculu
29	325.5	49.7	119	1	HV37_MOUSE	P01807 mus musculu
30	325.5	49.7	124	1	HV1D_HUMAN	P01760 homo sapien
31	324.5	49.5	119	1	HV38_MOUSE	P01808 mus musculu
32	323.5	49.4	119	1	HV40_MOUSE	P01810 mus musculu
33	320.5	48.9	122	1	HV3G_HUMAN	P01768 homo sapien
34	319	48.7	117	1	HV42_MOUSE	P01812 mus musculu
35	318.5	48.6	122	1	HV3A_HUMAN	P01762 homo sapien
36	318	48.5	121	1	HV3J_HUMAN	P01771 homo sapien
37	317	48.4	123	1	HV19_MOUSE	P01788 mus musculu
38	315	48.1	123	1	HV18_MOUSE	P01787 mus musculu
39	314.5	48.0	122	1	HV21_MOUSE	P01790 mus musculu
40	314	47.9	117	1	HV05_MOUSE	P01749 mus musculu
41	313	47.8	123	1	HV25_MOUSE	P01794 mus musculu
42	313	47.8	142	1	HV01_RAT	P01805 rattus norv
43	312	47.6	118	1	HV39_MOUSE	P01809 mus musculu
44	312	47.6	123	1	HV22_MOUSE	P01791 mus musculu
45	311.5	47.6	122	1	HV3H_HUMAN	P01769 homo sapien

ALIGNMENTS

RESULT 1
HV1C_HUMAN
ID HV1C_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE IG HEAVY CHAIN V-I REGION ND PRECURSOR (FRAGMENTS).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (In) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC PROTEIN.
DR PIR; A02026; E1HUND.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 16491 MW; 948F9F72A5366C20 CRC64;

Query Match 65.3%; Score 427.5; DB 1; Length 147;
Best Local Similarity 64.1%; Pred. No. 6.6e-36;
Matches 82; Conservative 16; Mismatches 25; Indels 5; Gaps 1;

```
Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           | |||||||||:||||||:|||||||:    |:||||:|||||  |||:| |:| :| | |
Db      20 QTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVGWINPNSGGTNY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-----EGYYGNYGVYAMDYWGQ 115
             |:|||||:| | | |||||:| ||||:|:||:|||:       ||     | :| |||
```

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Db      80 APRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAKSDPFWSDYYNFDYSYTLDVWGQ 139

Qy     116 GTLVTVSS 123
           || |||||
Db     140 GTTVTVSS 147


RESULT   2
HV03_MOUSE
ID   HV03_MOUSE     STANDARD;      PRT;   120 AA.
AC   P01747;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 36-65.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83131846; PubMed=6186498;
RA   Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA   Marshak-Rothstein A.;
RT   "The genetic basis of antibody production: the dominant anti-arsonate
RT   idiotype response of the strain A mouse.";
RL   Eur. J. Immunol. 12:1023-1032(1982).
CC   -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC       DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC       CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC       SEGMENT, JH2.
DR   PIR; A02028; HVMSG7.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13307 MW;  FF04E4A167B654AF CRC64;


  Query Match             62.4%;  Score 409;  DB 1;  Length 120;
  Best Local Similarity   63.1%;  Pred. No. 3.7e-34;
  Matches   77;  Conservative   18;  Mismatches   25;  Indels    2;  Gaps    1;

Qy       2 VQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYD 61
           ||| ||||| : |:|||:||||||:      |:||:| ||| |||:| |:| ||||||:
Db       1 VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN 60

Qy      62 PKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVTV 121
           ||:|: |:| | |:||||||:| || |||:|||:|||  |||  | |  ||||||| :||
Db      61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYG--GSYYFDYWGQGTTLTV 118

Qy     122 SS 123
           ||
Db     119 SS 120


RESULT   3
HV07_MOUSE
ID   HV07_MOUSE     STANDARD;      PRT;   139 AA.
AC   P01751; P01752;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J00529; AAA38170.1; -.
DR   PIR; A02034; MHMS18.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    139       IG HEAVY CHAIN V REGION B1-8/186-2.
FT   DOMAIN       20     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DOMAIN      118    124       D SEGMENT.
FT   DOMAIN      125    139       JH2 SEGMENT.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     139    139
SQ   SEQUENCE   139 AA;  15419 MW;  1B57DD4FD0C9F465 CRC64;


  Query Match             62.4%;  Score 408.5;  DB 1;  Length 139;
  Best Local Similarity   62.6%;  Pred. No. 4.9e-34;
  Matches   77;  Conservative   18;  Mismatches   25;  Indels    3;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| | |||: |||||||:||||||:     ::|||:| ||: |||:||||| :| |||
Db      20 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||: : |:| |  :|||||:|||| |||:|||||||  |||:     |||||| :|
Db      80 NEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGS---SYFDYWGQGTTLT 136

Qy     121 VSS 123
           |||
Db     137 VSS 139


RESULT   4
HV1B_HUMAN
ID   HV1B_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01743;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V-I REGION HG3 PRECURSOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83144028; PubMed=6298778;
RA   Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT   "Evolutionary aspects of immunoglobulin heavy chain variable region
```

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RT   (VH) gene subgroups.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------
DR   EMBL; J00240; AAA52988.1; -.
DR   PIR; A02024; HVHUHG.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    117       IG HEAVY CHAIN V-I REGION HG3.
FT   NON_TER    117    117
SQ   SEQUENCE   117 AA;  12946 MW;  2D3F92FC60CD1FE7 CRC64;


  Query Match             61.8%;  Score 405;  DB 1;  Length 117;
  Best Local Similarity   79.6%;  Pred. No. 9e-34;
  Matches   78;  Conservative    5;  Mismatches   15;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||||:     |:|||||||| ||||| |:|: | | |
Db      20 QVQLVQSGAEVKKPGASVKVSCKASGYTFNSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR 98
           |||||||:| ||| || ||||||||||||||||||||
Db      80 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR 117


RESULT   5
HV02_MOUSE
ID   HV02_MOUSE     STANDARD;      PRT;   140 AA.
AC   P01746;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/J;
RX   MEDLINE=82152818; PubMed=6801765;
RA   Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA   Capra J.D.;
RT   "Somatic mutation in genes for the variable portion of the
RT   immunoglobulin heavy chain.";
RL   Science 216:309-311(1982).
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00493; AAA38128.1; -.
DR   PIR; A02028; HVMSG7.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    140       IG HEAVY CHAIN V REGION 93G7.
FT   NON_TER    140    140
SQ   SEQUENCE   140 AA;  15514 MW;  25A4CBBE31DA5CE8 CRC64;


  Query Match             60.9%;  Score 399;  DB 1;  Length 140;
  Best Local Similarity   61.0%;  Pred. No. 4.4e-33;
  Matches   75;  Conservative   19;  Mismatches   27;  Indels    2;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: : |:|||:|||||:     |:||:| ||| |||:| |:| |||  |
Db      20 EVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYINY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||:|: |:| | |:|||||:| || |||:|||:|||  |||  | |  ||||||| :|
Db      80 NEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHYYG--GSYDFDYWGQGTPLT 137

Qy     121 VSS 123
           |||
Db     138 VSS 140


RESULT   6
HV1G_HUMAN
ID   HV1G_HUMAN     STANDARD;      PRT;   117 AA.
AC   P23083;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-NOV-1991 (Rel. 20, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V-I REGION V35 PRECURSOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88296408; PubMed=2841108;
RA   Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zong S.Q.,
RA   Ohno H., Fukuhara S., Honjo T.;
RT   "Dispersed localization of D segments in the human immunoglobulin
RT   heavy-chain locus.";
RL   EMBO J. 7:1047-1051(1988).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X07448; -; NOT_ANNOTATED_CDS.
DR   PIR; S00476; HVHU35.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    117       IG HEAVY CHAIN V-I REGION V35.
FT   NON_TER    117    117
SQ   SEQUENCE   117 AA;  13009 MW;  BE61CE63F8CE97BD CRC64;


  Query Match             60.5%;  Score 396;  DB 1;  Length 117;
  Best Local Similarity   78.6%;  Pred. No. 7.1e-33;
  Matches   77;  Conservative    5;  Mismatches   16;  Indels    0;  Gaps    0;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||||:     |:|||||||| ||||||:| :| | |
Db      20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGRINPNSGGTNY 79
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Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR 98
           ||||||| | ||| |||||||| |||:|| |||||||
Db      80 AQKFQGRVTSTRDTSISTAYMELSRLRSDDTVVYYCAR 117
```

RESULT 7
HV1A_HUMAN
ID HV1A_HUMAN STANDARD; PRT; 117 AA.
AC P01742;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-I REGION EU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS
CC MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
DR PIR; A02023; G1HUEU.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12472 MW; 99D60ADAEBD52818 CRC64;

Query Match 59.5%; Score 390; DB 1; Length 117;
Best Local Similarity 68.3%; Pred. No. 2.8e-32;
Matches 84; Conservative 8; Mismatches 25; Indels 6; Gaps 2;

```
Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||:||||||||||     : | ||||||||  ||||| | |  |    |
Db       1 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSRSAIIWVRQAPGQGLEWMGGIVPMFGPPNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||||||||| | :|||||||||||||||| |:||     | ||:|: : :  | |||
Db      61 AQKFQGRVTITADESTNTAYMELSSLRSEDTAFYFCA-----GGYGIYSPEEY-NGGLVT 114

Qy     121 VSS 123
           |||
Db     115 VSS 117
```

RESULT 8
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 57.7%; Score 378; DB 1; Length 117;
Best Local Similarity 58.5%; Pred. No. 4.4e-31;
Matches 72; Conservative 20; Mismatches 25; Indels 6; Gaps 1;

```
Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||| |: |||||||:||||||:   | |: ||:|: |: |||:| |:| || | |
Db       1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||:|: |:| | |:|||||:|:|| |||:|||||||: |      :  | || || ||
Db      61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY------WYFDVWGAGTTVT 114

Qy     121 VSS 123
           |||
Db     115 VSS 117
```

RESULT 9
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MHMS38.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

```
 Query Match             57.3%;  Score 375.5;  DB 1;  Length 118;
 Best Local Similarity   58.5%;  Pred. No. 8e-31;
 Matches   72;  Conservative   17;  Mismatches   29;  Indels    5;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||| |: |||||||:||||||:   | |::||:|: |: |||:| |:| || | |
Db       1 EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||:|: |:| | |:|  |||| || |||:|||||||      ||    | || || ||
Db      61 NQKFKGKATLTVDKSSSATYMELRSLTSEDSAVYYCAR-----GYGYDPFDVWGTGTTVT 115

Qy     121 VSS 123
           |||
Db     116 VSS 118


RESULT  10
HV12_MOUSE
ID   HV12_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01756;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION MOPC 104E.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83075344; PubMed=6816276;
RA   Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA   Hood L.E.;
RT   "Complete amino acid sequence of a mouse mu chain: homology among
RT   heavy chain constant region domains.";
RL   Biochemistry 21:5415-5424(1982).
CC   -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC       PROTEIN HAS ALSO BEEN DETERMINED.
CC   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR   PIR; A02039; MHMS4E.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Glycoprotein.
FT   DISULFID     22     96       BY SIMILARITY.
FT   CARBOHYD     55     55       N-LINKED (GLCNAC. . .).
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12983 MW;  3CF8ACE4BE447E41 CRC64;


  Query Match             56.9%;  Score 373;  DB 1;  Length 117;
  Best Local Similarity   59.3%;  Pred. No. 1.4e-30;
  Matches   73;  Conservative   19;  Mismatches   25;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||| |: |||||||:||||||:   | |: ||:|: |: |||:| |:| || | |
Db       1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||:|: |:| | |:|||||:|:|| |||:|||||||:     |  |  | || || ||
Db      61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARD-----YDWY-FDVWGAGTTVT 114

Qy     121 VSS 123
           |||
Db     115 VSS 117


RESULT  11
HV11_MOUSE
ID   HV11_MOUSE     STANDARD;      PRT;   137 AA.
AC   P01755;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00539; AAA38172.1; -.
DR   PIR; A02038; G2MS43.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    137       IG HEAVY CHAIN V REGION S43.
FT   DOMAIN      20     49       FRAMEWORK 1.
FT   DOMAIN      50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      55     68       FRAMEWORK 2.
FT   DOMAIN      69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      86    117       FRAMEWORK 3.
FT   DOMAIN     118    122       D SEGMENT.
FT   DOMAIN     123    137       JH2 SEGMENT.
FT   DISULFID    41    115       BY SIMILARITY.
FT   NON_TER    137    137
SQ   SEQUENCE   137 AA;  15200 MW;  ADD5881BF44B8EC9 CRC64;


  Query Match             56.7%;  Score 371.5;  DB 1;  Length 137;
  Best Local Similarity   60.2%;  Pred. No. 2.4e-30;
  Matches   74;  Conservative   14;  Mismatches   30;  Indels    5;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| | |||  |||||||:||||||:      :||| | ||: |||:|||||| :| | |
Db      20 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRPGRGLEWIGRIDPNSGGTTY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           :  |: : |:| |  :|||||:|||| |||:|||||||    | |     ||||||| :|
Db      80 NEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARY-RLGRY----FDYWGQGTTLT 134

Qy     121 VSS 123
           |||
Db     135 VSS 137


RESULT  12
HV48_MOUSE
ID   HV48_MOUSE     STANDARD;      PRT;   138 AA.
AC   P03980;
DT   23-OCT-1986 (Rel. 02, Created)
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DT   23-OCT-1986 (Rel. 02, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84248078; PubMed=6429663;
RA   Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA   Tucker P.W.;
RT   "Illegitimate recombination generates a class switch from C mu to C
RT   delta in an IgD-secreting plasmacytoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR   PIR; A02033; HVMST7.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    138       IG HEAVY CHAIN V REGION TEPC 1017.
FT   DOMAIN      21     49       FRAMEWORK 1.
FT   DOMAIN      50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      55     68       FRAMEWORK 2.
FT   DOMAIN      69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      86    117       FRAMEWORK 3.
FT   DOMAIN     118    127       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN     128    138       FRAMEWORK 4.
FT   DISULFID    41    115       BY SIMILARITY.
FT   NON_TER    138    138
SQ   SEQUENCE   138 AA;  15576 MW;  748157E4C6907B8E CRC64;
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  Query Match             56.3%;  Score 369;  DB 1;  Length 138;
  Best Local Similarity   58.1%;  Pred. No. 4.2e-30;
  Matches   72;  Conservative   20;  Mismatches   26;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| | |||: |||||::|||||     : :||||:| ||| |||:| |:| :| : |
Db      20 QVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRPGQGLEWIGEINPNDGRSNY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-EGYYGNYGVYAMDYWGQGTLV 119
           : ||: : |:| | |:|||||:|||| |: ||||||| :||| :      ||||||||
Db      80 NEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCARSDGYYDWF-----VYWGQGTLV 134

Qy     120 TVSS 123
           | |:
Db     135 TFSA 138
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RESULT  13
HV50_MOUSE
ID   HV50_MOUSE      STANDARD;      PRT;   120 AA.
AC   P06329;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION AC38 15.3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=84182519; PubMed=6201362;
RA   Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT   "A V region determinant (idiotope) expressed at high frequency in B
RT   lymphocytes is encoded by a large set of antibody structural genes.";
RL   EMBO J. 3:517-523(1984).
DR   PIR; A02037; MHMS15.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN       1     98       V SEGMENT.
FT   DOMAIN      99    105       D SEGMENT.
FT   DOMAIN     106    120       J SEGMENT.
FT   DISULFID    22     96       BY SIMILARITY.
FT   NON_TER    120    120
SQ   SEQUENCE   120 AA;  13311 MW;  914453F426F09834 CRC64;
```

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  Query Match             55.6%;  Score 364.5;  DB 1;  Length 120;
  Best Local Similarity   56.1%;  Pred. No. 1e-29;
  Matches   69;  Conservative   19;  Mismatches   32;  Indels    3;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||:| | |: |||||| :|||||||:     ::||:|| ||| |||:| |:|:|| | |
Db       1 QVQLLQPGTELVKPGASVNLSCKASGYTFTSYWMHWIRQRPGQGLEWIGGINPSNGGTNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||: : |:| | |:|  ||:||:  |||:|||||||  | |:       | || || ||
Db      61 NEKFKSKATLTVDKSSSATYMQLSTPTSEDSAVYYCARWDYEGD---RYFDVWGTGTTVT 117

Qy     121 VSS 123
           |||
Db     118 VSS 120
```

```
RESULT  14
HV01_MOUSE
ID   HV01_MOUSE      STANDARD;      PRT;   121 AA.
AC   P01745;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION MPC 11.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81053741; PubMed=6253904;
RA   Zakut R., Cohen J., Givol D.;
RT   "Cloning and sequence of the cDNA corresponding to the variable
RT   region of immunoglobulin heavy chain MPC11.";
RL   Nucleic Acids Res. 8:3591-3601(1980).
RN   [2]
RP   REVISIONS.
RA   Zakut R., Cohen J., Givol D.;
RL   Nucleic Acids Res. 8:4839-4840(1980).
CC   -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC       FROM A MYELOMA THAT SECRETES IGG2B.
DR   PIR; A02027; GVMS11.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13135 MW;  227AEF3EC56ED0BF CRC64;
```

```
  Query Match             55.0%;  Score 360;  DB 1;  Length 121;
  Best Local Similarity   55.3%;  Pred. No. 2.9e-29;
  Matches   68;  Conservative   23;  Mismatches   30;  Indels    2;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           : || |||||: :|| |||:||||:|:|:    : :| ||:: ||  |||:| | |  |:| |
Db       1 EAQLQQSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
```

```
          :   :|: |:|||||:||||::|||| |||:|:|:||| | | |   |  | |||||  :|
Db      61 NDNLKGKATLTADTSSSTAYIQLSSLTSEDSAIYHCAR-GIYYNSSPY-FDSWGQGTTLT 118

Qy     121 VSS 123
           |||
Db     119 VSS 121


RESULT  15
HV15_MOUSE
ID   HV15_MOUSE     STANDARD;      PRT;   136 AA.
AC   P01759;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION BCL1 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82222262; PubMed=6806821;
RA   Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA   Blattner F.R.;
RT   "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT   by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT   by two adjacent CH genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00494; AAA38130.1; -.
DR   PIR; A02042; HVMSB1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    136       IG HEAVY CHAIN V REGION BCL1.
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  15078 MW;  6827CFBC6DB3F35E CRC64;


  Query Match             55.0%;  Score 360;  DB 1;  Length 136;
  Best Local Similarity   56.9%;  Pred. No. 3.3e-29;
  Matches   70;  Conservative   17;  Mismatches   30;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| ||| || :|| |||:||| ||:   |  :|||:|:  : |||:| |   || | |
Db      20 QVQLQQSGPEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSHAKSLEWIGVISTYNGNTSY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||:|: |:| | |:|| :||| | |||:|  ||||  |||||     ||||||| :|
Db      80 NQKFKGKATMTVDKSSSTVHMELARLTSEDSANLYCAR--YYGNY----FDYWGQGTTLT 133

Qy     121 VSS 123
           |||
Db     134 VSS 136


Search completed: May  7, 2002, 12:32:34
Job time: 565 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:31:42 ; Search time 67.26 Seconds
(without alignments)
267.492 Million cell updates/sec

Title: US-09-155-739-11
Perfect score: 655
Sequence: 1 QVQLVQSGAEVKKPGASVKV.....NYGVYAMDYWGQGTLVTVSS 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	457.5	69.8	124	4	Q9UL92	Q9ul92 homo sapien
2	440	67.2	468	11	Q99L31	Q99131 mus musculu
3	432	66.0	109	11	Q9JL85	Q9j185 mus musculu
4	432	66.0	119	4	Q9UL94	Q9ul94 homo sapien
5	428	65.3	119	5	Q9GYZ2	Q9gyz2 schistosoma
6	428	65.3	125	4	Q9UL95	Q9ul95 homo sapien
7	422	64.4	473	11	Q9D8L4	Q9d814 mus musculu
8	411.5	62.8	116	4	Q9UL89	Q9ul89 homo sapien
9	408.5	62.4	473	11	Q99L25	Q99125 mus musculu
10	407	62.1	117	11	Q9QXE9	Q9qxe9 mus musculu
11	399	60.9	150	4	Q9Y298	Q9y298 homo sapien
12	398.5	60.8	500	4	Q9BRV0	Q9brv0 homo sapien
13	386.5	59.0	118	11	Q9Z1C4	Q9z1c4 mus musculu
14	386	58.9	117	11	Q9QXF0	Q9qxf0 mus musculu
15	384	58.6	157	4	O95978	O95978 homo sapien
16	381.5	58.2	463	11	Q99LC4	Q99lc4 mus musculu
17	380	58.0	484	11	Q99LA6	Q99la6 mus musculu
18	379.5	57.9	109	11	Q9JL75	Q9j175 mus musculu
19	374.5	57.2	110	11	Q9JL77	Q9j177 mus musculu
20	371.5	56.7	114	11	Q9JL81	Q9j181 mus musculu
21	342.5	52.3	110	11	Q9JL83	Q9j183 mus musculu
22	338	51.6	111	11	Q9D9B8	Q9d9b8 mus musculu
23	334	51.0	117	11	Q9Z1C6	Q9z1c6 mus musculu
24	333	50.8	120	4	Q9BUA1	Q9bua1 homo sapien
25	326.5	49.8	487	11	Q99KA4	Q99ka4 mus musculu
26	325.5	49.7	298	11	Q9QYF0	Q9qyf0 mus musculu
27	322.5	49.2	147	4	Q9Y509	Q9y509 homo sapien
28	322	49.2	113	4	Q9UL90	Q9ul90 homo sapien
29	320.5	48.9	118	4	Q9UL72	Q9ul72 homo sapien
30	319.5	48.8	112	4	Q9HCC1	Q9hcc1 homo sapien
31	314	47.9	116	4	Q9UL93	Q9ul93 homo sapien
32	311	47.5	131	4	Q9UL88	Q9ul88 homo sapien
33	304	46.4	121	4	Q9UL71	Q9ul71 homo sapien
34	300.5	45.9	121	11	Q99NG4	Q99ng4 mus musculu
35	297.5	45.4	122	4	Q9UL84	Q9ul84 homo sapien
36	290	44.3	119	4	Q9UL73	Q9ul73 homo sapien
37	288.5	44.0	124	6	Q9N0W4	Q9n0w4 oryctolagus
38	286.5	43.7	118	4	Q9UL91	Q9ul91 homo sapien
39	286	43.7	597	4	Q9BQB8	Q9bqb8 homo sapien
40	285.5	43.6	124	6	Q9N0W6	Q9n0w6 oryctolagus
41	285	43.5	597	4	Q9BU10	Q9bu10 homo sapien
42	279	42.6	104	4	Q9UL87	Q9ul87 homo sapien
43	275	42.0	479	11	Q99M22	Q99m22 mus musculu
44	273.5	41.8	437	11	Q9R1A4	Q9r1a4 mus musculu
45	271	41.4	102	11	Q9JL79	Q9j179 mus musculu

ALIGNMENTS

```
RESULT   1
Q9UL92
ID   Q9UL92      PRELIMINARY;      PRT;   124 AA.
AC   Q9UL92;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035022; AAD56258.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     124    124
SQ   SEQUENCE   124 AA;  13580 MW;  1BAAACBD96ACD2A2 CRC64;

  Query Match          69.8%;  Score 457.5;  DB 4;  Length 124;
  Best Local Similarity   69.5%;  Pred. No. 5.1e-40;
  Matches   91;  Conservative    9;  Mismatches   16;  Indels   15;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||||:||||||||||||||||||||:     |:|||||||| ||||| |:|: | | |
Db       1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAM--------DY 112
           |||||||:| ||| || ||||||||||||||||||||       |:| :         ||
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Db      61 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR-------GLYVVVPAAFSRFDY 113

Qy     113 WGQGTLVTVSS 123
           ||||||||||||
Db     114 WGQGTLVTVSS 124


RESULT   2
Q99L31
ID   Q99L31      PRELIMINARY;      PRT;   468 AA.
AC   Q99L31;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003878; AAH03878.1; -.
SQ   SEQUENCE   468 AA;  51661 MW;  96352328B3332ADB CRC64;


  Query Match             67.2%;  Score 440;  DB 11;  Length 468;
  Best Local Similarity   67.5%;  Pred. No. 1.7e-37;
  Matches   83;  Conservative   16;  Mismatches   20;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| |||||: :||||||:|| |||||||| :|||:| | | |||:| ||| :| |||
Db      20 EVQLQQSGAELVRPGASVKLSCTASGFNIKDSLMHWVKQRPEQGLEWIGWIDPEDGETKY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           |||| : ||||||::|||::|||| ||||||||||    || |     |||||| :|
Db      80 APKFQDKATITADTSSNTAYLQLSSLTSEDTAIYYCARNLLYGGY----YDYWGQGTTIT 135

Qy     121 VSS 123
           |||
Db     136 VSS 138


RESULT   3
Q9JL85
ID   Q9JL85      PRELIMINARY;      PRT;   109 AA.
AC   Q9JL85;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206021; AAF69319.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11944 MW;  DFE615FE6CED4EDE CRC64;


  Query Match             66.0%;  Score 432;  DB 11;  Length 109;
  Best Local Similarity   68.7%;  Pred. No. 1.9e-37;
  Matches   79;  Conservative   15;  Mismatches   15;  Indels    6;  Gaps    1;

Qy       9 AEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYDPKFQGRV 68
           ||: ||||||:|| |||||:|||:|||:| | | |||:|||||| |::|||||||:
Db       1 AELVKPGASVKLSCTASGFNIEDTYMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKA 60

Qy      69 TITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVTVSS 123
           |||:|||::|||::|||| |||||||||| |       |    ||||||| :||||
Db      61 TITSDTSSNTAYLQLSSLTSEDTAVYYCVRR------GAVVFDYWGQGTALTVSS 109


RESULT   4
Q9UL94
ID   Q9UL94      PRELIMINARY;      PRT;   119 AA.
AC   Q9UL94;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035020; AAD56256.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13205 MW;  13E64F5345F4A16E CRC64;


  Query Match             66.0%;  Score 432;  DB 4;  Length 119;
  Best Local Similarity   70.7%;  Pred. No. 2.1e-37;
  Matches   87;  Conservative   10;  Mismatches   22;  Indels    4;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||||:||||||||||||||||||||:     |:|||||||| ||||| |:| :  | |
Db       1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSWTTNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           ||||:||:| ||| |||||||| |||:|||||||| |  | :     | ||||||||
Db      61 AQKFQGKVTMTKDTSISTAYMELSRLRSDDTAVYYCARGGGRGLW----FDPWGQGTLVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119


RESULT   5
Q9GYZ2
ID   Q9GYZ2      PRELIMINARY;      PRT;   119 AA.
AC   Q9GYZ2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 HEAVY CHAIN VARIABLE REGION
DE   (FRAGMENT).
```

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OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC   Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC   Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song X.T., Feng Z.Q., Guan X.H.;
RT   "Amplification, cloning and sequence analysis of the heavy chain
RT   variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT   Schistosoma japonicum.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF282622; AAG01452.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13567 MW;  BA893873FD5FA6AB CRC64;

  Query Match             65.3%;  Score 428;  DB 5;  Length 119;
  Best Local Similarity   66.7%;  Pred. No. 5.5e-37;
  Matches   82;  Conservative   17;  Mismatches   20;  Indels    4;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||:|||||:||||||:|||||||:     |::|||||||  |||:| |:|: ||| |
Db       1 QVQLVESGAEVRKPGASVRVSCKASGYTFTGYYMNWVRQAPGHGLEWIGYINPSRGYTNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||: |||:| | | ||||||:| |||| |:||||||||  || ::  | :|||||||  ||
Db      61 NQKFKDRVTMTTDKSFSTAYMDLRSLRSADSAVYYCAR--YYDDH--YCLDYWGQGTTVT 116

Qy     121 VSS 123
           |||
Db     117 VSS 119


RESULT   6
Q9UL95
ID   Q9UL95       PRELIMINARY;      PRT;   125 AA.
AC   Q9UL95;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035019; AAD56255.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     125    125
SQ   SEQUENCE   125 AA;  13516 MW;  0D3CD5C232488EAC CRC64;

  Query Match             65.3%;  Score 428;  DB 4;  Length 125;
  Best Local Similarity   68.8%;  Pred. No. 5.9e-37;
  Matches   86;  Conservative   10;  Mismatches   27;  Indels    2;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :|||:|||||||||||||||||||:     |:|||||||| ||||| |:| :| | |
Db       1 EVQLVESGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMGWINPNSGGTNY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY--AMDYWGQGTL 118
             | |||||:| ||: |||||||| |||:|||||||||     |       | | |||||:
Db      61 AQKVQGRVTMTRDTTISTAYMELSRLRSDDTAVYYCARSQGGGRIAAAGDAFDIWGQGTM 120

Qy     119 VTVSS 123
           |||||
Db     121 VTVSS 125


RESULT   7
Q9D8L4
ID   Q9D8L4       PRELIMINARY;      PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   1810060O09RIK PROTEIN.
GN   1810060O09RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AK007918; BAB25349.1; -.
DR   MGD; MGI:1924014; 1810060O09Rik.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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SQ   SEQUENCE   473 AA;  51699 MW;  9DED57A514475FBB CRC64;

  Query Match             64.4%;  Score 422;  DB 11;  Length 473;
  Best Local Similarity   65.9%;  Pred. No. 1.3e-35;
  Matches   81;  Conservative   19;  Mismatches   19;  Indels    4;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| |||||: ||||||:|||||:    | ||:||:| ||| |||:|:| | :| | |
Db      20 QVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRPGQGLEWIGKIGPGSGSTYY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||:|: |:||| |:|||||:|||| |||:|||:||| ||  :|  :|  |||||||||
Db      80 NEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGY--DYDWFA--YWGQGTLVT 135

Qy     121 VSS 123
           |||
Db     136 VSA 138


RESULT   8
Q9UL89
ID   Q9UL89       PRELIMINARY;      PRT;   116 AA.
AC   Q9UL89;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035025; AAD56261.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    116    116
SQ   SEQUENCE   116 AA;  12605 MW;  C8F9131DE13EA898 CRC64;

  Query Match             62.8%;  Score 411.5;  DB 4;  Length 116;
  Best Local Similarity   72.5%;  Pred. No. 2.8e-35;
  Matches   87;  Conservative    3;  Mismatches   25;  Indels    5;  Gaps    2;

Qy       5 VQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKYDPKF 64
           ||||||||||:|||||||||       | |||||||| ||||||| |  |   |  ||
Db       1 VQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGRIIPILGIANYAQKF 60

Qy      65 QGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVY-AMDYWGQGTLVTVSS 123
           ||||||||| | ||||||||||||||||||||      |:| |   | ||:||||||||
Db      61 QGRVTITADKSTSTAYMELSSLRSEDTAVYYCAS----SNWGPYWYFDLWGRGTLVTVSS 116


RESULT   9
Q99L25
ID   Q99L25       PRELIMINARY;      PRT;   473 AA.
AC   Q99L25;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003888; AAH03888.1; -.
SQ   SEQUENCE   473 AA;  52449 MW;  BE9889B7986DA155 CRC64;

  Query Match             62.4%;  Score 408.5;  DB 11;  Length 473;
  Best Local Similarity   63.2%;  Pred. No. 3.2e-34;
  Matches   79;  Conservative   18;  Mismatches   25;  Indels    3;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||| || ||: |||||||:||| ||:   |  ||||:| | | |||:| | | :| |||
Db      20 QVQLQQSDAELVKPGASVKISCKVSGYTFTDHTIHWVKQRPEQGLEWIGYIYPRDGSTKY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREG--YYGNYGVYAMDYWGQGTL 118
           : ||:|: |:||| |:|||||:|:|| |||:|| :|:| |  ||| ||:|  |||||||
Db      80 NEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGGSIYYG-YGLYYFDYWGQGTT 138

Qy     119 VTVSS 123
           :|||
Db     139 ITVSS 143


RESULT  10
Q9QXE9
ID   Q9QXE9       PRELIMINARY;      PRT;   117 AA.
AC   Q9QXE9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AJ225174; CAB65237.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER      1      1
FT   NON_TER    117    117
SQ   SEQUENCE   117 AA;  13000 MW;  CDDE2AF84D499734 CRC64;

  Query Match             62.1%;  Score 407;  DB 11;  Length 117;
  Best Local Similarity   62.6%;  Pred. No. 8.1e-35;
  Matches   77;  Conservative   19;  Mismatches   21;  Indels    6;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||| |: |||||||:||||||:    | |: ||:|: |: |||:| |:| || | |
Db       1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
           : ||:|: |:| | |:||||||:|:|| |||:|||||||: |      ||||||||| ||
Db      61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY------YAMDYWGQGTSVT 114

Qy     121 VSS 123
           |||
Db     115 VSS 117
```

```
RESULT  11
Q9Y298
ID   Q9Y298      PRELIMINARY;      PRT;   150 AA.
AC   Q9Y298;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   IGG VH PROTEIN PRECURSOR (FRAGMENT).
GN   IGG VH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98322155; PubMed=9657749;
RA   Jacquemin M.G., Vander Elst L.P.L.;
RT   "Mechanism and kinetics of factor VIII inactivation: study with an
RT   IgG4 monoclonal antibody derived from a hemophilia A patient with
RT   inhibitor.";
RL   Blood 92:496-506(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AJ224083; CAA11829.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   NON_TER     150    150
SQ   SEQUENCE   150 AA;  16031 MW;  563D164AB22802D5 CRC64;


  Query Match             60.9%;  Score 399;  DB 4;  Length 150;
  Best Local Similarity   65.0%;  Pred. No. 7.5e-34;
  Matches   80;  Conservative   12;  Mismatches   25;  Indels    6;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||||||||||||||||||||||| ||: : :  :||| |||| : |||:|  || :| : |
Db      20 QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAPGKGLEWVGSFDPESGESIY 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120
             :||| ||:|||||   |||||||||:|||||||           | | |||||:||
Db      80 AREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVP------DPDAFDIWGQGTMVT 133

Qy     121 VSS 123
           |||
Db     134 VSS 136


RESULT  12
Q9BRV0
ID   Q9BRV0      PRELIMINARY;      PRT;   500 AA.
AC   Q9BRV0;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   UNKNOWN (PROTEIN FOR MGC:14588).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PROSTATE;
RA   Strausberg R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005951; AAH05951.1; -.
SQ   SEQUENCE   500 AA;  54154 MW;  0A9BF43F2A3CC6D9 CRC64;


  Query Match             60.8%;  Score 398.5;  DB 4;  Length 500;
  Best Local Similarity   63.3%;  Pred. No. 3.7e-33;
  Matches   81;  Conservative   10;  Mismatches   32;  Indels    5;  Gaps    1;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           || |||||||  |||||:|||| ||:      | |||||||| ||||| | |::  |::
Db      20 QVHLVQSGAEVMSPGASVRVSCKTSGYAFHTYSIIWVRQAPGQGLEWMGWISPSSDNTRF 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAR-----EGYYGNYGVYAMDYWGQ 115
             |||||||:| ||| || |||| ||||:|||||||||          :|  | || ||:
Db      80 AKKFQGRVTLTTDTSTSTVYMELRSLRSDDTAVYYCARRYCSYSSCQNDYYYYYMDVWGK 139

Qy     116 GTLVTVSS 123
           || |||||
Db     140 GTTVTVSS 147


RESULT  13
Q9Z1C4
ID   Q9Z1C4      PRELIMINARY;      PRT;   118 AA.
AC   Q9Z1C4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA   Matis L.M., Evans M.J.;
RT   "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT   IgG2/G4 constant regions block human leukocyte binding to porcine
RT   endothelial cells.";
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; U78801; AAD00293.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13036 MW;  90EEC559D31EC4FC CRC64;


  Query Match             59.0%;  Score 386.5;  DB 11;  Length 118;
  Best Local Similarity   59.5%;  Pred. No. 1.1e-32;
  Matches   75;  Conservative   18;  Mismatches   22;  Indels   11;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           |||: ||||| : | ||||:|||||:|    :: ||:| ||| |||:| | | :| | |
Db       1 QVQVQQSGAELARPWASVKLSCKASGYNFNSYWMQWVKQRPGQGLEWIGAIYPGDGDTSY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE---GYYGNYGVYAMDYWGQGT 117
             ||:|: |:||| |:|||||:|||| |||:|||||||    ||:        |||||||
Db      61 TQKFRGKATLTADKSSSTAYMQLSSLASEDSAVYYCARRTVGGYF--------DYWGQGT 112

Qy     118 LVTVSS 123
           :||||
Db     113 TLTVSS 118


RESULT  14
Q9QXF0
ID   Q9QXF0      PRELIMINARY;      PRT;   117 AA.
AC   Q9QXF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
```

```
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AJ225171; CAB65236.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13060 MW;  D816AD0858A47E4C CRC64;
```

```
  Query Match             58.9%;  Score 386;  DB 11;  Length 117;
  Best Local Similarity   59.7%;  Pred. No. 1.2e-32;
  Matches   74;  Conservative   20;  Mismatches   22;  Indels    8;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           :||| ||| |: ||||||:|||||:   | |: ||:|: |: |||:| |:| || | |
Db       1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCARE-GYYGNYGVYAMDYWGQGTLV 119
           : ||:|: |:| | |:|||||:|:|| |||:|||||||:  ||        ||||||| :
Db      61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDKDYY-------FDYWGQGTTL 113

Qy     120 TVSS 123
           ||||
Db     114 TVSS 117
```

```
RESULT  15
O95978
ID   O95978      PRELIMINARY;      PRT;   157 AA.
AC   O95978;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   VH1 PROTEIN PRECURSOR (FRAGMENT).
GN   VH1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PERIPHERAL BLOOD;
RA   Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,
RA   Bohlen H., Diehl V., Wolf J.;
RT   "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT   patient with mixed cellularity Hodgkin's disease is associated with
RT   somatic mutations within the untranslated regions of rearranged and
RT   class switch recombinated Ig genes.";
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AJ005570; CAA06599.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   NON_TER     157    157
SQ   SEQUENCE   157 AA;  17304 MW;  86986EDDA84D88B5 CRC64;
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  Query Match             58.6%;  Score 384;  DB 4;  Length 157;
  Best Local Similarity   63.2%;  Pred. No. 2.8e-32;
  Matches   79;  Conservative   10;  Mismatches   30;  Indels    6;  Gaps    2;

Qy       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60
           ||||||||||:|:|||||| || ||:     |||||| || ||||| | |  | |
Db      20 QVQLVQSGAEIKRPGASVKVHCKTSGYVFTSYYIHWVRQPRGQGLEWMGGIGPGVGSTMC 79

Qy      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYY--GNYGVYAMDYWGQGTL 118
             |||||:|:| :|| :| ||||| || ||||||:| | | :  |||      :|||||
Db      80 AEKFQGRLTMTRNTSTTTVYMELSRLRFEDTAVYFCGRGGRWRSGNYN----GHWGQGTP 135

Qy     119 VTVSS 123
           |||||
Db     136 VTVSS 140
```

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Search completed: May  7, 2002, 12:31:42
Job time: 628 sec
```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:18:19 ; Search time 67.39 Seconds
(without alignments)
138.496 Million cell updates/sec

Title: US-09-155-739-2
Perfect score: 680
Sequence: 1 MRPSIQFLGLLLFWLHGAQC.....YCLQYDNLWTFGGGTKLEIK 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101:*
1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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10: /SIDS8/gcgdata/geneseq/geneseqp/AA1989.DAT:*
11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
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22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	680	100.0	126	16	AAR81326	Mouse VLA-4 antibo
2	680	100.0	126	16	AAR81332	Human VLA-4 reshap
3	680	100.0	126	18	AAW22409	Alpha-4 integrin m
4	634	93.2	128	15	AAR60627	ME1-14 light chain
5	619	91.0	126	18	AAW22419	Humanised alpha-4
6	618.5	91.0	128	11	AAR06252	Variable region of
7	569	83.7	106	16	AAR81328	Mouse anti-VLA-4 a
8	539	79.3	359	20	AAY29913	Human MCP-3 and mu
9	539	79.3	361	20	AAY29911	Human IP-10 and mu
10	535	78.7	374	20	AAY29916	Artificial synthet
11	510.5	75.1	107	16	AAR78970	Light chain variab
12	508	74.7	106	16	AAR81321	Humanized anti-VLA
13	508	74.7	106	18	AAW22412	Humanised alpha-4
14	508	74.7	108	17	AAR93159	Murine monoclonal
15	508	74.7	637	13	AAR26983	(FRP51)-ETA fusion
16	507	74.6	245	19	AAW26800	Anti-gp54 MAb T16
17	503	74.0	109	19	AAW26797	Anti-gp54 MAb T16
18	503	74.0	240	16	AAR85495	ScFv(FWP51). Synt
19	501	73.7	355	18	AAW35133	R. pipiens recombi
20	500	73.5	109	12	AAR13658	Murine OKT4A light
21	500	73.5	241	13	AAR26981	FWP51 fusion prote
22	479.5	70.5	234	12	AAR13050	CD4-specific CDR-g
23	464.5	68.3	128	22	AAB81995	Ganglioside GD3 sp
24	462.5	68.0	234	18	AAW10233	TF8-5G9 CDR-grafte
25	457.5	67.3	128	22	AAB81996	Ganglioside GD3 sp
26	456.5	67.1	129	15	AAR57482	Humanized 1308F VL
27	456.5	67.1	129	17	AAR92085	Humanised antibody
28	455.5	67.0	129	15	AAR47207	Human/murine IL-1
29	452.5	66.5	128	22	AAB81997	Ganglioside GD3 sp
30	451.5	66.4	127	12	AAR12359	Light (kappa) chai
31	451.5	66.4	129	21	AAY56724	Amino acid sequenc
32	448.5	66.0	128	22	AAB81993	Ganglioside GD3 sp
33	447.5	65.8	129	19	AAW70379	Anti-human CD23 5E
34	446.5	65.7	126	12	AAR12237	Mouse MAb 1C11 L c
35	446.5	65.7	129	14	AAR30880	pXOM2. Mus muscul
36	445.5	65.5	132	18	AAW22842	Human anti-tumour
37	443.5	65.2	130	21	AAY56737	Amino acid sequenc
38	442	65.0	124	21	AAY56719	Amino acid sequenc
39	441	64.9	237	21	AAY96301	Human IGFAM-13 imm
40	438.5	64.5	128	17	AAW01527	Monoclonal antibod
41	438.5	64.5	128	18	AAW24990	Monoclonal antibod
42	437.5	64.3	127	14	AAR39265	Mouse C4G1 Ig ligh
43	437.5	64.3	127	19	AAW49809	Variable region of
44	437.5	64.3	131	16	AAR84553	MAb SCH94.03 light
45	436.5	64.2	128	22	AAB81999	Ganglioside GD3 sp

ALIGNMENTS

RESULT 1
AAR81326
ID AAR81326 standard; Protein; 126 AA.
XX
AC AAR81326;
XX
DT 23-MAR-1996 (first entry)
XX
DE Mouse VLA-4 antibody 21.6 light chain variable region.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.
XX
OS Mus musculus.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1..20
FT		/note= "signal peptide"
FT	Region	21..43
FT		/note= "framework region 1"
FT	Region	44..54
FT		/note= "complementarity determining region 1"
FT	Region	55..69
FT		/note= "framework region 2"
FT	Region	70..76
FT		/note= "complementarity determining region 2"
FT	Region	77..108
FT		/note= "framework region 3"
FT	Region	109..116
FT		/note= "complementarity determining region 3"
FT	Region	117..126
FT		/note= "framework region 4"

XX
PN WO9519790-A1.

XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
DR N-PSDB; AAQ99889.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating
PT inflammatory disease.
XX
PS Disclosure; Fig 1; 105pp; English.
XX
CC The sequence represents the mouse antibody 21.6 light chain variable
CC region directed against leukocyte adhesion molecule VLA-4. Cloned
CC cDNA sequences of mouse 21.6 VL and VH (see AAQ99892) regions are
CC linked to human constant regions in the construction of a humanized
CC antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC modified using PCR primers (See AAQ99895-98) and then subcloned into
CC mammalian cell expression vectors containing human kappa or gamma-1
CC constant regions. In the humanized light chain, amino acids L45,
CC L49, L58 and L69 in the human kappa LC VR framework are replaced
CC by the amino acid present in the equivalent position of the mouse
CC 21.6 Ig L chain. Plasmids encoding the chimeric antibodies are
CC transfected into COS cells. The humanized antibodies can be used
CC to inhibit adhesion of a leukocyte to an endothelial cell and
CC to treat inflammatory diseases such as multiple sclerosis. They
CC can also be used in the treatment of stroke, cerebral traumas,
CC meningitis or encephalitis. The antibodies can also be used for
CC detecting VLA-4, for affinity purification or for generating
CC anti-idiotype antibodies.
XX
SQ Sequence 126 AA;

Query Match 100.0%; Score 680; DB 16; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.2e-47;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mrpsiqflgllfwlhgaqcdiqmtqspsslsaslggkvtitcktsqdinkymawyqhkp 60

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 gkrprllihytsalqpgipsrfsgsgsgrdysfnisnlepediatyyclqydnlwtfggg 120

Qy     121 TKLEIK 126
           ||||||
Db     121 tkleik 126
```

RESULT 2
AAR81332
ID AAR81332 standard; Protein; 126 AA.
XX
AC AAR81332;
XX
DT 23-MAR-1996 (first entry)
XX
DE Human VLA-4 reshaped antibody 21.6 light chain variable region.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "signal peptide"
FT Region 21..43
FT /note= "framework region 1"
FT Region 44..54
FT /note= "complementarity determining region 1"
FT Region 55..69
FT /note= "framework region 2"
FT Region 70..76
FT /note= "complementarity determining region 2"
FT Region 77..108
FT /note= "framework region 3"
FT Region 109..116
FT /note= "complementarity determining region 3"
FT Region 117..126
FT /note= "framework region 4"
XX
PN WO9519790-A1.
XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
DR N-PSDB; AAQ99893.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating
PT inflammatory disease.
XX
PS Disclosure; Fig 10; 105pp; English.
XX
CC The sequence represents the human reshaped antibody 21.6 light
CC chain variable region against leukocyte adhesion molecule VLA-4.
CC Cloned cDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892)
CC regions are linked to human constant regions in the construction
CC of a humanized antibody against VLA-4. The 5' and 3' ends of the
CC mouse cDNAs are modified using PCR primers (See AAQ99895-98) and
CC then subcloned into mammalian cell expression vectors containing
CC human kappa or gamma-1 constant regions. In the humanized light
CC chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR
CC framework are replaced by the amino acid present in the equivalent
CC position of the mouse 21.6 Ig L chain. Plasmids encoding the
CC chimeric antibodies are transfected into COS cells. The humanized
CC antibodies can be used to inhibit adhesion of a leukocyte to an
CC endothelial cell and to treat inflammatory diseases such as
CC multiple sclerosis. They can also be used in the treatment of
CC stroke, cerebral traumas, meningitis or encephalitis. The
CC antibodies can also be used for detecting VLA-4, for affinity
CC purification or for generating anti-idiotype antibodies.
XX
SQ Sequence 126 AA;

Query Match 100.0%; Score 680; DB 16; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.2e-47;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mrpsiqflgllfwlhgaqcdiqmtqspsslsaslggkvtitcktsqdinkymawyqhkp 60

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 gkrprllihytsalqpgipsrfsgsgsgrdysfnisnlepediatyyclqydnlwtfggg 120
```

```
Qy     121 TKLEIK 126
           ||||||
Db     121 tkleik 126


RESULT   3
AAW22409
ID   AAW22409 standard; Protein; 126 AA.
XX
AC   AAW22409;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Alpha-4 integrin mouse MAb 21.6 VL region.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Leader
FT   Region          21..43
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /label= FR3
FT                   /note= "framework region 3"
FT   Region          109..116
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Region          117..126
FT                   /label= FR4
FT                   /note= "framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones ST,  Leger OJ,  Saldanha J,  Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74759.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 18; Page 68; 107pp; English.
XX
CC   This polypeptide comprises the light chain variable region (VL) of
CC   mouse anti-alpha-4 integrin monoclonal antibody 21.6.  The
CC   complementarity determining regions (CDRs) of the 21.6 VL can be
CC   incorporated into a human REI framework to produce a claimed
CC   humanised 21.6 VL (see AAW22412) and a claimed humanised 21.6
CC   antibody that is used in the manufacture of a medicament for
CC   treating a disease selected from asthma, atherosclerosis, AIDS,
CC   dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury.  The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen.  It is also useful for
CC   generating idiotypic antibodies.  The humanised antibodies of the
CC   invention have a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   126 AA;


  Query Match             100.0%;  Score 680;  DB 18;  Length 126;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-47;
  Matches  126;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mrpsiqflglllfwlhgaqcdiqmtqspsslsaslggkvtitcktsqdinkymawyqhkp 60

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 gkrprllihytsalqpgipsrfsgsgsgrdysfnisnlepediatyyclqydnlwtfggg 120

Qy     121 TKLEIK 126
           ||||||
Db     121 tkleik 126


RESULT   4
AAR60627
ID   AAR60627 standard; Protein; 128 AA.
XX
AC   AAR60627;
XX
DT   04-JUN-1995  (first entry)
XX
DE   ME1-14 light chain variable region.
XX
KW   Monoclonal antibody; tumour.
XX
OS   Homo sapiens.
XX
PN   WO9421294-A.
XX
PD   29-SEP-1994.
XX
PF   14-MAR-1994;   94WO-US02724.
XX
PR   19-MAR-1993;   93US-0033864.
XX
PA   (BIGN/) BIGNER D D.
PA   (CARR/) CARREL S.
PA   (ZALU/) ZALUTSKY M R.
XX
PI   Bigner DD,  Carrel S,  Zalutsky MR;
XX
DR   WPI; 1994-316669/39.
DR   N-PSDB; AAQ73537.
XX
PT   Method of treating solid or cystic tumours with antibodies - by
PT   administering monoclonal antibody Mel-14, having Fc deleted,
PT   using injection or deposition in the cyst cavity
XX
PS   Disclosure; Fig 2; 31pp; English.
XX
CC   The sequence is that of the ME1-14 light chain.  The protein is  a
CC   monoclonal antibody which can be administered to treat solid or
```

```
CC   cystic tumours.
CC   See also AAR60626.
XX
SQ   Sequence   128 AA;


  Query Match             93.2%;  Score 634;  DB 15;  Length 128;
  Best Local Similarity   93.7%;  Pred. No. 5.9e-44;
  Matches  118;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           |||||||||||||||||| |||||||||||||||||||||||| |||||||:|||||||
Db       1 mrpsiqflglllfwlhgahcdiqmtqspsslsaslggkvtitckasqdinkyiawyqhkp 60

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
           || ||||:|||| |||||||||||||||||:||||||||||||||||||| |||||
Db      61 gkgprllmhytstlqpgipsrfsgsgsgrdysfsisnlepediatyyclqydnlltfggg 120

Qy     121 TKLEIK 126
           ||||||
Db     121 tkleik 126


RESULT   5
AAW22419
ID   AAW22419 standard; Protein; 126 AA.
XX
AC   AAW22419;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL version La.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Leader
FT   Protein         21..126
FT                   /label= Mat_protein
FT                   /note= "VL version La (Claim 25)"
FT   Region          21..43
FT                   /label= FR1
FT                   /note= "REI framework region 1"
FT   Region          44..54
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          55..69
FT                   /label= FR2
FT                   /note= "REI framework region 2"
FT   Region          70..76
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          77..108
FT                   /label= FR3
FT                   /note= "REI framework region 3"
FT   Region          109..116
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Region          117..126
FT                   /label= FR4
FT                   /note= "REI framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones ST,  Leger OJ,  Saldanha J,  Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74788.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Fig 10; 107pp; English.
XX
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also
CC   AAW22412).  It is composed of complementarity determining regions from
CC   the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal
CC   antibody 21.6 and a modified human REI framework.  It can be
CC   expressed in mammalian host cells following PCR amplification and
CC   mutagenesis of appropriate mouse and human DNA sequences.  The
CC   humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury.  The humanised
CC   antibody has a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   126 AA;


  Query Match             91.0%;  Score 619;  DB 18;  Length 126;
  Best Local Similarity   90.5%;  Pred. No. 9.2e-43;
  Matches  114;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           |||||||||||||||||||||||||||||||:| :|||||||||||||||||  |
Db       1 mrpsiqflglllfwlhgaqcdiqmtqspsslsasvgdrvtitcktsqdinkymawyqqtp 60

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
           || |||||||||||||||||||||||:| ||:|:|||||||||||||||||| |
Db      61 gkaprllihytsalqpgipsrfsgsgsgrdytftisslqpediatyyclqydnlwtfgqg 120

Qy     121 TKLEIK 126
           ||:|||
Db     121 tkveik 126


RESULT   6
AAR06252
ID   AAR06252 standard; protein; 128 AA.
XX
AC   AAR06252;
XX
DT   10-DEC-1990  (first entry)
XX
DE   Variable region of murine AHT 107 light chain.
XX
KW   Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
XX
OS   Mus sp.
XX
PN   EP380068-A.
XX
PD   01-AUG-1990.
```

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XX
PF   24-JAN-1990;   90EP-0101351.
XX
PR   04-DEC-1989;   89US-0441702.
PR   24-JAN-1989;   89US-0301216.
XX
PA   (MOLE-) MOLECULAR THERAPEU.
XX
PI   Zerler B;
XX
DR   WPI; 1990-232892/31.
DR   N-PSDB; AAQ05556.
XX
PT   Expression vectors for producing chimeric monoclonal antibodies -
PT   which express human constant region and non-human variable region
XX
PS   Disclosure; ; p; English.
XX
CC   MAbs comprising mouse CH and CL constant regions whith human
CC   variable regions may be used to create mouse/human hybrid MAbs,
CC   which have a longer serum half-life. Method can be used to produce
CC   Abs against interleukin-2 receptor and tumour necrosis factor.
XX
SQ   Sequence   128 AA;


  Query Match             91.0%;  Score 618.5;  DB 11;  Length 128;
  Best Local Similarity   88.2%;  Pred. No. 1e-42;
  Matches  112;  Conservative   12;  Mismatches    2;  Indels    1;  Gaps    1;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           |||||||||||||||||||||||||||||||||||||||:||||||||||::|||||||
Db       1 mrpsiqflgllfwlhgaqcdiqmtqspsslsaslggkvtltcktsqdinkfiawyqhkp 60

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
           |: |||:||||| |||||||||||||:||||:|:||||||||||||:||:| |||||
Db      61 gegprliihytstlqpgipsrfsgsgsgkdysfsinnlepediatyyclryddlpwtfgg 120

Qy     120 GTKLEIK 126
           |||||::
Db     121 gtklevr 127


RESULT   7
AAR81328
ID   AAR81328 standard; Protein; 106 AA.
XX
AC   AAR81328;
XX
DT   02-APR-1996  (first entry)
XX
DE   Mouse anti-VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Region          1..23
FT                   /label= FR1
FT                   /note= "mouse light chain variable framework
FT                        region 1"
FT   Region          24..34
FT                   /label= CDR1
FT                   /note= "mouse light chain variable complementarity
FT                        determining region 1"
FT   Region          35..49
FT                   /label= FR2
FT                   /note= "mouse light chain variable framework
FT                        region 2"
FT   Region          50..56
FT                   /label= CDR2
FT                   /note= "mouse light chain variable complementarity
FT                        determining region 2"
FT   Region          57..88
FT                   /label= FR3
FT                   /note= "mouse light chain variable framework
FT                        region 3"
FT   Region          89..96
FT                   /label= CDR3
FT                   /note= "mouse light chain variable complementarity
FT                        determining region 3"
FT   Region          97..106
FT                   /label= FR4
FT                   /note= "mouse light chain variable framework
FT                        region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Page 66; 105pp; English.
XX
CC   The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain
CC   variable region (without signal sequence). Cloned cDNA CDR sequences of
CC   mouse 21.6 variable light and variable heavy regions are linked to human
CC   constant framework regions of the REI antibody for the light chain and
CC   the 2*CL antibody for the heavy chain in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45, L49,
CC   L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC   acid present in the equivalent position of the mouse 21.6 Ig light
CC   chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC   cells. The humanized antibodies can be used to inhibit adhesion of a
CC   leukocyte to an endothelial cell and to treat inflammatory diseases such
CC   as multiple sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC   used for detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   106 AA;


  Query Match             83.7%;  Score 569;  DB 16;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 8e-39;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 diqmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           ||||||||||||||||||||||||||||||||||||||||||||||
Db      61 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 106


RESULT   8
AAY29913
ID   AAY29913 standard; Protein; 359 AA.
```

XX
AC AAY29913;
XX
DT 17-NOV-1999 (first entry)
XX
DE Human MCP-3 and murine scFv38 fusion protein.
XX
KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW immune response; HIV; infection.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
PN WO9946392-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05345.
XX
PR 12-MAR-1998; 98US-0077745.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kwak LW, Biragyn A;
XX
DR WPI; 1999-551418/46.
XX
PT New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection -
XX
PS Disclosure; Page 118-119; 142pp; English.
XX
CC The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC be used for producing an immune response, e.g. an effector T cell immune
CC response. They can also be used for treating cancer or treating or
CC preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC can be used in in vitro diagnostic assays, as well as in screening assays
CC for identifying unknown tumour antigen epitopes and fine mapping of
CC tumour antigen epitopes. The present sequence represents a fusion protein
CC from the present invention.
XX
SQ Sequence 359 AA;

Query Match 79.3%; Score 539; DB 20; Length 359;
Best Local Similarity 91.8%; Pred. No. 6.7e-36;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
|: |||||||||||||||||||||| ||||||:||||||||| ||||||||| |||
Db 229 gsgsdiqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqp 288

Qy 77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
||||||||||||||||:||||||||||||||||||:||||||||||
Db 289 gipsrfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 338

RESULT 9
AAY29911
ID AAY29911 standard; Protein; 361 AA.
XX
AC AAY29911;
XX
DT 17-NOV-1999 (first entry)
XX
DE Human IP-10 and murine scFv38 fusion protein.
XX
KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW immune response; HIV; infection.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
PN WO9946392-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05345.
XX
PR 12-MAR-1998; 98US-0077745.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kwak LW, Biragyn A;
XX
DR WPI; 1999-551418/46.
XX
PT New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection -
XX
PS Disclosure; Page 115-116; 142pp; English.
XX
CC The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC be used for producing an immune response, e.g. an effector T cell immune
CC response. They can also be used for treating cancer or treating or
CC preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC can be used in in vitro diagnostic assays, as well as in screening assays
CC for identifying unknown tumour antigen epitopes and fine mapping of
CC tumour antigen epitopes. The present sequence represents a fusion protein
CC from the present invention.
XX
SQ Sequence 361 AA;

Query Match 79.3%; Score 539; DB 20; Length 361;
Best Local Similarity 91.8%; Pred. No. 6.7e-36;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
|: |||||||||||||||||||||| ||||||:||||||||| ||||||||| |||
Db 231 gsgsdiqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqp 290

Qy 77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
||||||||||||||||:||||||||||||||||||:||||||||||
Db 291 gipsrfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 340

RESULT 10
AAY29916
ID AAY29916 standard; Protein; 374 AA.
XX
AC AAY29916;
XX
DT 17-NOV-1999 (first entry)
XX
DE Artificial synthetic construct protein SEQ ID NO:15.
XX
KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;

KW immune response; HIV; infection.
XX
OS Synthetic.
XX
PN WO9946392-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05345.
XX
PR 12-MAR-1998; 98US-0077745.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kwak LW, Biragyn A;
XX
DR WPI; 1999-551418/46.
XX
PT New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection -
XX
PS Disclosure; Page 117-118; 142pp; English.
XX
CC The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion
CC proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and
CC human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human
CC Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)
CC human SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human
CC MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and
CC HIV gp120. The fusion proteins, and nucleotide sequences encoding them,
CC can be used for producing an immune response, e.g. an effector T cell
CC immune response. They can also be used for treating cancer or treating
CC or preventing HIV infection. The fusion proteins and/or nucleotide
CC sequences can be used in in vitro diagnostic assays, as well as in
CC screening assays for identifying unknown tumour antigen epitopes and fine
CC mapping of tumour antigen epitopes. AAY29916 and AAZ21156 to AAZ21168 are
CC sequences given in the SEQ ID LISTING in the present invention but which
CC are not mentioned further within the specification.
XX
SQ Sequence 374 AA;

Query Match 78.7%; Score 535; DB 20; Length 374;
Best Local Similarity 94.3%; Pred. No. 1.5e-35;
Matches 100; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           ||||||||||||||||||||||| ||||||:||||||||| ||||||||| |||||||
Db      95 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 154

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           |||||||||||||:|||||||||||||||||||:||||||||||
Db     155 rfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 200
```

RESULT 11
AAR78970
ID AAR78970 standard; Protein; 107 AA.
XX
AC AAR78970;
XX
DT 21-DEC-1995 (first entry)
XX
DE Light chain variable region for monoclonal antibody 23F8.
XX
KW Monoclonal antibody; heavy metal; mercury; variable region;
KW light chain.
XX
OS Synthetic.
XX
PN WO9520607-A.
XX
PD 03-AUG-1995.
XX
PF 27-JAN-1995; 95WO-US01199.
XX
PR 27-JAN-1994; 94US-0187407.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Lopez O, Wagner FW, Wylie DE;
XX
DR WPI; 1995-275415/36.
DR N-PSDB; AAQ97508.
XX
PT New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT monoclonal antibodies, used for detecting, removing, adding or
PT neutralising heavy metals
XX
PS Claim 23; Page 67-68; 106pp; English.
XX
CC Hybridoma antibodies have been produced with the spleen cells of
CC BALB/c mouse that had received multiple injections of mercuric ions
CC reacted with glutathione to produce a mercuric ion coordinate
CC covalent compound which was covalently bound to keyhole limpet
CC hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC 5B6 and 3E8) were producing MAbs that were strongly positive
CC against glutatione-mercuric ions but negative against glutathione
CC without mercuric ions. RNA was isolated from hybridoma cells with
CC guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC were complementary to the 5' end of the CH1 domain of the heavy
CC chain expressed by the hybridoma of interest, or to the 5' and of
CC the C kappa domain. Some of the primers used for cDNA synthesis are
CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
CC variable region of a particular antibody polypeptide was also used
CC for PCR amplification of that variable region, in conjunction with
CC an appropriate V-region primer. In addition, the VH primer AAQ97518
CC was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC of the PCR amplified nucleotides were determined. These are given
CC in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
CC AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC and in the claims are different from the descriptions in the
CC sequence listings. The descriptions in the sequence listings are
CC used here.
XX
SQ Sequence 107 AA;

Query Match 75.1%; Score 510.5; DB 16; Length 107;
Best Local Similarity 91.6%; Pred. No. 4e-34;
Matches 98; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

```
Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||||||||||| ||||||:||||||||| ||||||||| |||||||
Db       1 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
           |||||||||||||:||| |||||||||||||| |:||| |||||||
Db      61 rfsgsgsgrdysfsisnpepediatyyclqydnslftfgsgtkleik 107
```

RESULT 12
AAR81321
ID AAR81321 standard; Protein; 106 AA.
XX
AC AAR81321;
XX
DT 02-APR-1996 (first entry)
XX
DE Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.

XX
OS Chimeric Mus musculus.
OS Chimeric Homo sapiens.
XX
PN WO9519790-A1.
XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating
PT inflammatory disease.
XX
PS Claim 9; Page 67; 105pp; English.
XX
CC The sequence encodes the humanized mouse antibody 21.6 light chain
CC variable region, La, directed against leukocyte adhesion molecule
CC VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and
CC AAQ99892) regions are linked to human constant regions in the
CC construction of a humanized antibody against VLA-4. The 5' and 3'
CC ends of the mouse cDNAs are modified using PCR primers (See
CC AAQ99895-98) and then subcloned into mammalian cell expression vectors
CC containing human kappa or gamma-1 constant regions. In the humanized
CC light chain, amino acids L45, L49, L58 and L69 in the human kappa LC
CC VR framework are replaced by the amino acid present in the equivalent
CC position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric
CC antibodies are transfected into COS cells. The humanized antibodies
CC can be used for inhibiting adhesion of a leukocyte to an endothelial
CC cell and for treating inflammatory diseases such as multiple
CC sclerosis. They can also be used in the treatment of stroke,
CC cerebral traumas, meningitis or encephalitis. The antibodies can
CC also be used for detecting VLA-4, for affinity purification or for
CC generating anti-idiotype antibodies.
XX
SQ Sequence 106 AA;

Query Match 74.7%; Score 508; DB 16; Length 106;
Best Local Similarity 88.7%; Pred. No. 6.3e-34;
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

```
Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           ||||||||||||||:| :|||||||||||||||||||  ||| ||||||||||||||||
Db       1 diqmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           |||||||||||:| ||:|:|||||||||||||||||||| |||:|||
Db      61 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 106
```

RESULT 13
AAW22412
ID AAW22412 standard; Protein; 106 AA.
XX
AC AAW22412;
XX
DT 08-DEC-1997 (first entry)
XX
DE Humanised alpha-4 integrin antibody 21.6 VL La.
XX
KW Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW transplant rejection; graft versus host disease; nephritis;
KW atopic dermatitis; psoriasis; myocardial ischaemia;
KW acute leukocyte mediated lung injury; therapy.
XX
OS Chimeric Mus musculus;
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
XX

FH	Key	Location/Qualifiers
FT	Region	1..23
FT		/label= FR1
FT		/note= "REI framework region 1"
FT	Region	24..34
FT		/label= CDR1
FT		/note= "21.6 complementarity determining region 1"
FT	Region	35..49
FT		/label= FR2
FT		/note= "REI framework region 2"
FT	Misc-difference	45
FT		/note= "REI Lys-45 is substd. by Lys of mouse
FT		21.6 VL, important in supporting the
FT		CDR2 loop"
FT	Misc-difference	49
FT		/note= "REI Tyr-49 is substd. by His of mouse
FT		21.6 VL, located at the binding site"
FT	Region	50..56
FT		/label= CDR2
FT		/note= "21.6 complementarity determining region 2"
FT	Region	57..88
FT		/label= FR3
FT		/note= "REI framework region 3"
FT	Misc-difference	58
FT		/note= "REI Val-58 is substd. by Ile of mouse
FT		21.6 VL, important in supporting the CDR2
FT		loop"
FT	Misc-difference	69
FT		/note= "REI Thr-69 is substd. by Arg of mouse
FT		21.6 VL, involved in antibody-antigen
FT		binding"
FT	Region	89..96
FT		/label= CDR3
FT		/note= "21.6 complementarity determining region 3"
FT	Region	97..106
FT		/label= FR4
FT		/note= "REI framework region 4"
FT	Misc-difference	103
FT		/note= "REI Leu-103 substd. by Val, more typical
FT		of human kappa light chain J region"
FT	Misc-difference	104
FT		/note= "REI Gln-104 substd. by Glu, more typical
FT		of human kappa light chain J region"
FT	Misc-difference	106
FT		/note= "REI Thr-106 substd. by Lys, more typical
FT		of human kappa light chain J region"

XX
PN WO9718838-A1.
XX
PD 29-MAY-1997.
XX
PF 21-NOV-1996; 96WO-US18807.
XX
PR 21-NOV-1995; 95US-0561521.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR WPI; 1997-297879/27.
XX
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS Claim 25; Fig 6; 107pp; English.
XX

```
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6.  It is
CC   composed of complementarity determining regions (CDRs) from the VL
CC   region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody
CC   21.6 and a modified human REI framework.  It can be expressed in
CC   mammalian host cells following PCR amplification and mutagenesis
CC   of appropriate fragments of mouse and human DNA sequences.  The
CC   humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury.  The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen.  It is also useful for
CC   generating idiotypic antibodies.  The humanised antibody has a
CC   half-life in the human circulation essentially equivalent to that
CC   of naturally occurring human antibodies.
XX
SQ   Sequence   106 AA;


  Query Match             74.7%;  Score 508;  DB 18;  Length 106;
  Best Local Similarity   88.7%;  Pred. No. 6.3e-34;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           ||||||||||||||:| :||||||||||||||||||  ||| ||||||||||||||||||
Db       1 diqmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           |||||||||||:| ||:|:||||||||||||||||||| |||:|||
Db      61 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 106


RESULT  14
AAR93159
ID   AAR93159 standard; Protein; 108 AA.
XX
AC   AAR93159;
XX
DT   24-OCT-1996  (first entry)
XX
DE   Murine monoclonal antibody K20 kappa chain variable region.
XX
KW   Antibody; light chain; kappa; variable region; K20; integrin; CD29;
KW   beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
KW   T cell activation; complementarity determining region; CDR.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Region          1..23
FT                   /label= FR1
FT                   /note= "framework region"
FT   Region          24..34
FT                   /label= CDR1
FT                   /note= "complementarity determining region"
FT   Region          35..49
FT                   /label= FR2
FT                   /note= "framework region"
FT   Region          50..56
FT                   /label= CDR2
FT                   /note= "complementarity determining region"
FT   Region          57..88
FT                   /label= FR3
FT                   /note= "framework region"
FT   Region          89..94
FT                   /label= CDR3
FT                   /note= "complementarity determining region"
FT   Region          95..108
FT                   /label= J_kappa1
XX
PN   FR2724393-A1.
XX
PD   15-MAR-1996.
XX
PF   12-SEP-1994;   94FR-0010858.
XX
PR   12-SEP-1994;   94FR-0010858.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (PROT-) PROTEINE PERFORMANCE SA.
XX
PI   Bernard A,  Cervoni MF,  Lefranc MP,  Margaritte C;
PI   Poul MA;
XX
DR   WPI; 1996-162083/17.
DR   N-PSDB; AAT26849.
XX
PT   Humanisation of non-human immunoglobulin variable regions - for
PT   prodn. of humanised antibodies, esp. K20, e.g. as an
PT   immunosuppressant
XX
PS   Example 1; Fig 2A; 39pp; French.
XX
CC   The present sequence is that of the variable region of the kappa
CC   light chain from murine monoclonal antibody K20. The antibody
CC   recognises the beta 1 subunit (CD29) of integrins and inhibits
CC   activation and proliferation of peripheral T cells induced by
CC   anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target
CC   for humanisation; the humanised version may be useful as an
CC   immunosuppressant. In the humanisation process, the complementarity
CC   determining regions (CDRs) of a human antibody with framework
CC   regions 70-95% homologous to those of K20 were replaced by the K20
CC   CDRs.
XX
SQ   Sequence   108 AA;


  Query Match             74.7%;  Score 508;  DB 17;  Length 108;
  Best Local Similarity   89.6%;  Pred. No. 6.4e-34;
  Matches   95;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||:|||||||||||||||||| |||||||:|||||:||| ||||| ||| |: ||||
Db       1 diqltqspsslsaslggkvtitckasqdinkyiawyqhepgkgprllirytsklesgips 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           |||||||||||||:|||||||||||||||| ||||||||||||||
Db      61 rfsgsgsgrdysfsisnlepediatyyclqyynlwtfgggtkleik 106


RESULT  15
AAR26983
ID   AAR26983 standard; Protein; 637 AA.
XX
AC   AAR26983;
XX
DT   11-FEB-1993  (first entry)
XX
DE   (FRP51)-ETA fusion protein.
XX
KW   Monoclonal antibody; light chain; heavy chain; tumour; c-erbB-2;
KW   variable region; ETA.
XX
OS   Pseudomonas aeruginosa.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..21
FT                   /label= ompA_signal_peptide
FT   Peptide         22..29
FT                   /label= FLAG_peptide_and_enterokinase_cleavage_site
FT   Domain          33..152
FT                   /label= FWP51_heavy_chain_variable_domain
```

FT Peptide 153..167
FT /label= Linker
FT Domain 168..274
FT /label= FRP5_light_chain_variable_domain
FT Protein 276..397
FT /label= ETA_252-613
XX
PN EP502812-A.
XX
PD 09-SEP-1992.
XX
PF 27-JAN-1992; 92EP-0810056.
XX
PR 05-FEB-1991; 91EP-0810079.
XX
PA (CIBA) CIBA GEIGY AG.
XX
PI Groner B, Hardman N, Harwerth I, Hynes NE, Wels WS;
PI Zwickl M;
XX
DR WPI; 1992-302096/37.
DR N-PSDB; AAQ28263.
XX
PT Recombinant antibodies directed to growth factor receptor C-erbB-2 -
PT for diagnosing and treating tumours expressing C-erbB-2 e.g. breast
PT or ovarian tumours
XX
PS Disclosure; Page 53-58; 67pp; English.
XX
CC The sequences given in AAR26982-3 contain part of the exotoxin A (ETA)
CC sequence corresponding to positions 252-613 of the full exotoxin A
CC sequence. These sequences are encoded by Fv(FRP5)-ETA fusion genes.
CC The ETA sequence was used as a marker gene so that E. coli transformed
CC with the fusion gene could be identified. The fusion genes were
CC expressed in E. coli and the antibodies were extracted. These
CC recombinant antibodies can be used for the qualitative and
CC quantitative determination of c-erbB-2. This can be used for
CC monitoring or in-vivo localisation of tumours overexpressing c-erbB-2.
XX
SQ Sequence 637 AA;

Query Match 74.7%; Score 508; DB 13; Length 637;
Best Local Similarity 86.4%; Pred. No. 3.6e-33;
Matches 95; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

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Qy      17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
           |   |||:||||||||||||||:|||||| |||| ||:|||||||||| ||||||||| |||
Db     164 gggsdiqltqspsslsaslggevtitckasqdikkyiawyqhkpgksprllihytsvlqp 223

Qy      77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           |||||||||||||||||:| |||||||||||| || |:||||||||||
Db     224 gipsrfsgsgsgrdysfsihnlepediatyyclhydylytfgggtkleik 273
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Search completed: May 7, 2002, 12:22:24
Job time: 245 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:20:09 ; Search time 32.41 Seconds
(without alignments)
87.486 Million cell updates/sec

Title: US-09-155-739-2
Perfect score: 680
Sequence: 1 MRPSIQFLGLLLFWLHGAQC.....YCLQYDNLWTFGGGTKLEIK 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	680	100.0	126	2	US-08-561-521-2	Sequence 2, Appli
2	680	100.0	126	2	US-08-561-521-15	Sequence 15, Appl
3	680	100.0	126	5	PCT-US95-01219-2	Sequence 2, Appli
4	680	100.0	126	5	PCT-US95-01219-15	Sequence 15, Appl
5	634	93.2	128	1	US-08-339-582-4	Sequence 4, Appli
6	569	83.7	106	2	US-08-561-521-5	Sequence 5, Appli
7	569	83.7	106	5	PCT-US95-01219-5	Sequence 5, Appli
8	510.5	75.1	107	2	US-08-888-366-22	Sequence 22, Appl
9	508	74.7	106	2	US-08-561-521-7	Sequence 7, Appli
10	508	74.7	106	5	PCT-US95-01219-7	Sequence 7, Appli
11	508	74.7	637	1	US-08-235-838-16	Sequence 16, Appl
12	508	74.7	637	2	US-08-465-473B-16	Sequence 16, Appl
13	503	74.0	241	1	US-08-235-838-11	Sequence 11, Appl
14	503	74.0	241	2	US-08-465-473B-11	Sequence 11, Appl
15	501	73.7	355	3	US-08-875-811-57	Sequence 57, Appl
16	438.5	64.5	128	1	US-08-259-372A-14	Sequence 14, Appl
17	438.5	64.5	128	1	US-08-468-671-14	Sequence 14, Appl
18	437.5	64.3	127	1	US-08-458-516-5	Sequence 5, Appli
19	437.5	64.3	127	4	US-08-348-548-4	Sequence 4, Appli
20	437.5	64.3	127	5	PCT-US95-15716-4	Sequence 4, Appli
21	437.5	64.3	131	1	US-08-236-520-2	Sequence 2, Appli
22	437.5	64.3	131	5	PCT-US95-05262-2	Sequence 2, Appli
23	430.5	63.3	138	2	US-08-480-434-63	Sequence 63, Appl
24	430.5	63.3	138	2	US-08-053-451B-63	Sequence 63, Appl
25	429.5	63.2	127	3	US-08-836-561-71	Sequence 71, Appl
26	428.5	63.0	129	1	US-08-217-918-2	Sequence 2, Appli
27	426.5	62.7	127	1	US-08-137-117D-37	Sequence 37, Appl
28	426.5	62.7	127	2	US-08-436-717-37	Sequence 37, Appl
29	424.5	62.4	127	3	US-08-649-100-17	Sequence 17, Appl
30	423.5	62.3	236	1	US-08-157-101A-5	Sequence 5, Appli
31	418.5	61.5	142	2	US-08-579-940-2	Sequence 2, Appli
32	418.5	61.5	142	4	US-08-838-692-4	Sequence 4, Appli
33	417.5	61.4	127	1	US-08-137-117D-29	Sequence 29, Appl
34	417.5	61.4	127	2	US-08-436-717-29	Sequence 29, Appl
35	417.5	61.4	127	3	US-08-933-983-7	Sequence 7, Appli
36	416.5	61.2	127	2	US-08-621-751A-6	Sequence 6, Appli
37	416.5	61.2	127	3	US-08-836-561-88	Sequence 88, Appl
38	414.5	61.0	128	2	US-08-470-139-26	Sequence 26, Appl
39	413.5	60.8	125	2	US-08-039-198B-12	Sequence 12, Appl
40	413.5	60.8	125	2	US-08-182-067-2	Sequence 2, Appli
41	413.5	60.8	125	2	US-08-465-313-2	Sequence 2, Appli
42	413.5	60.8	127	3	US-08-649-100-33	Sequence 33, Appl
43	412.5	60.7	127	4	US-09-136-315-8	Sequence 8, Appli
44	410.5	60.4	127	3	US-08-933-983-17	Sequence 17, Appl
45	410.5	60.4	128	4	US-08-569-147-80	Sequence 80, Appl

ALIGNMENTS

```
RESULT 1
US-08-561-521-2
; Sequence 2, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-2


  Query Match           100.0%;  Score 680;  DB 2;  Length 126;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-59;
  Matches  126;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60

Qy     61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120

Qy    121 TKLEIK 126
          ||||||
Db    121 TKLEIK 126
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RESULT 2
US-08-561-521-15
; Sequence 15, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-15

Query Match 100.0%; Score 680; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.3e-59;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60

Qy     61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120

Qy    121 TKLEIK 126
          ||||||
Db    121 TKLEIK 126
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RESULT 3
PCT-US95-01219-2
; Sequence 2, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 126 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-2

Query Match 100.0%; Score 680; DB 5; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.3e-59;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60

Qy     61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120

Qy    121 TKLEIK 126
          ||||||
Db    121 TKLEIK 126
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RESULT 4
PCT-US95-01219-15
; Sequence 15, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.

```
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-15


  Query Match             100.0%;  Score 680;  DB 5;  Length 126;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-59;
  Matches  126;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120

Qy     121 TKLEIK 126
           ||||||
Db     121 TKLEIK 126


RESULT   5
US-08-339-582-4
; Sequence 4, Application US/08339582
; Patent No. 5558852
;  GENERAL INFORMATION:
;    APPLICANT:  Bigner, Darell D.
;    APPLICANT:  Zalutsky, Michael R.
;    APPLICANT:  Carrel, Stefan
;    TITLE OF INVENTION:  METHOD OF TREATMENT
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  P.O. Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 5558852th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/339,582
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/033,864
;      FILING DATE:  19-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5405-89
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  128 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-339-582-4


  Query Match             93.2%;  Score 634;  DB 1;  Length 128;
  Best Local Similarity   93.7%;  Pred. No. 4.2e-55;
  Matches  118;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           |||||||||||||||||| |||||||||||||||||||||||| |||||||:|||||||
Db       1 MRPSIQFLGLLLFWLHGAHCDIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKP 60

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
           || ||||:|||| ||||||||||||||||||:||||||||||||||||| |||||
Db      61 GKGPRLLMHYTSTLQPGIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLLTFGGG 120

Qy     121 TKLEIK 126
           ||||||
Db     121 TKLEIK 126


RESULT   6
US-08-561-521-5
; Sequence 5, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
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;       FILING DATE:
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/186,269A
;       FILING DATE:  25-JAN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William L.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  15270-14
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-543-9600
;       TELEFAX:  415-543-5043
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  106 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-561-521-5


  Query Match             83.7%;  Score 569;  DB 2;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-49;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106


RESULT   7
PCT-US95-01219-5
; Sequence 5, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  106 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-5


  Query Match             83.7%;  Score 569;  DB 5;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-49;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106


RESULT   8
US-08-888-366-22
; Sequence 22, Application US/08888366
; Patent No. 5972656
;  GENERAL INFORMATION:
;    APPLICANT:  Lopez, Osvaldo
;    APPLICANT:  Wylie, Dwane E.
;    APPLICANT:  Wagner, Fred W.
;    TITLE OF INVENTION:  Mercury Binding Polypeptides and Nucleotides Coding Therefo
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  90 South 7th Street, 3100 No. 5972656west Ctr.
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,366
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/187,407
;      FILING DATE:  27-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,542
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/493,299
;      FILING DATE:  14-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/324,392
;      FILING DATE:  14-MAR-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carter, Charles G.
;      REGISTRATION NUMBER:  35,093
;      REFERENCE/DOCKET NUMBER:  8648.39USC1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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US-08-888-366-22

Query Match 75.1%; Score 510.5; DB 2; Length 107;
Best Local Similarity 91.6%; Pred. No. 4.1e-43;
Matches 98; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

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Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           ||||||||||||||||||||||||| ||||||:||||||||| ||||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN-LWTFGGGTKLEIK 126
           |||||||||||||:||| |||||||||||||| |:||| |||||||
Db      61 RFSGSGSGRDYSFSISNPEPEDIATYYCLQYDNSLFTFGSGTKLEIK 107
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RESULT 9
US-08-561-521-7
; Sequence 7, Application US/08561521
; Patent No. 5840299
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/561,521
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,269A
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-561-521-7

Query Match 74.7%; Score 508; DB 2; Length 106;
Best Local Similarity 88.7%; Pred. No. 7e-43;
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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           ||||||||||||||:| :||||||||||||||||||  ||| ||||||||||||||||
Db       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           ||||||||||||:| ||:|:|||||||||||||||||| |||:|||
Db      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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RESULT 10
PCT-US95-01219-7
; Sequence 7, Application PC/TUS9501219
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Leger, Olivier J.
; APPLICANT: Saldanha, Jose
; APPLICANT: Jones, S. Tarran
; TITLE OF INVENTION: Humanized Antibodies Against Leukocyte
; TITLE OF INVENTION: Adhesion Molecule VLA-4
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01219
; FILING DATE: 25-JAN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/186,269
; FILING DATE: 25-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William L.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15270-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-01219-7

Query Match 74.7%; Score 508; DB 5; Length 106;
Best Local Similarity 88.7%; Pred. No. 7e-43;
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
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Db       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           ||||||||||||:| ||:|:|||||||||||||||||| |||:|||
Db      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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RESULT 11
US-08-235-838-16
; Sequence 16, Application US/08235838
; Patent No. 5571894
; GENERAL INFORMATION:
; APPLICANT: Wels, Winfried S.
; APPLICANT: Hynes, Nancy E.
; APPLICANT: Harwerth, Ina-Maria
; APPLICANT: Groner, Bernd

```
;    APPLICANT:  Hardman, No. 5571894man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CIBA-GEIGY Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/235,838
;      FILING DATE:  TBA
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elmer, James Scott
;      REGISTRATION NUMBER:  36,129
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)541-8614
;      TELEFAX:  (919)541-8689
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-235-838-16


  Query Match             74.7%;  Score 508;  DB 1;  Length 637;
  Best Local Similarity   86.4%;  Pred. No. 5.8e-42;
  Matches   95;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy      17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
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Db     164 GGGSDIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 223

Qy      77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           ||||||||||||||||:| |||||||||||| || |:||||||||||
Db     224 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273


RESULT  12
US-08-465-473B-16
; Sequence 16, Application US/08465473B
; Patent No. 5939531
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5939531man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NOVARTIS Corporation
;      STREET:  564 Morris Avenue
;      CITY:  Summit
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07901-6940
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,473B
;      FILING DATE:  5 June 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pfeiffer, Hesna J.
;      REGISTRATION NUMBER:  22,640
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)522 6940
;      TELEFAX:  (908)522 6955
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-465-473B-16


  Query Match             74.7%;  Score 508;  DB 2;  Length 637;
  Best Local Similarity   86.4%;  Pred. No. 5.8e-42;
  Matches   95;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy      17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
           |   |||:|||||||||||||:|||||| |||| ||:|||||||| ||||||||| |||
Db     164 GGGSDIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 223

Qy      77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           ||||||||||||||||:| |||||||||||| || |:||||||||||
Db     224 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273


RESULT  13
US-08-235-838-11
; Sequence 11, Application US/08235838
; Patent No. 5571894
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5571894man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CIBA-GEIGY Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/235,838
;       FILING DATE:  TBA
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/828,832
;       FILING DATE:  31-JAN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  GB 91-810079.3
;       FILING DATE:  05-FEB-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Elmer, James Scott
;       REGISTRATION NUMBER:  36,129
;       REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (919)541-8614
;       TELEFAX:  (919)541-8689
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  241 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-235-838-11


  Query Match             74.0%;  Score 503;  DB 1;  Length 241;
  Best Local Similarity   86.2%;  Pred. No. 5.7e-42;
  Matches   94;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy      17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
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Db     133 GGGSDIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 192

Qy      77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEI 125
           ||||||||||||||||:| |||||||||||| || |:||||||||||
Db     193 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241


RESULT  14
US-08-465-473B-11
; Sequence 11, Application US/08465473B
; Patent No. 5939531
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5939531man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NOVARTIS Corporation
;      STREET:  564 Morris Avenue
;      CITY:  Summit
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07901-6940
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,473B
;      FILING DATE:  5 June 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pfeiffer, Hesna J.
;      REGISTRATION NUMBER:  22,640
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)522 6940
;      TELEFAX:  (908)522 6955
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  241 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-465-473B-11


  Query Match             74.0%;  Score 503;  DB 2;  Length 241;
  Best Local Similarity   86.2%;  Pred. No. 5.7e-42;
  Matches   94;  Conservative    5;  Mismatches   10;  Indels    0;  Gaps    0;

Qy      17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
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Db     133 GGGSDIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQP 192

Qy      77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEI 125
           ||||||||||||||||:| |||||||||||| || |:||||||||||
Db     193 GIPSRFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241


RESULT  15
US-08-875-811-57
; Sequence 57, Application US/08875811
; Patent No. 6045793
;  GENERAL INFORMATION:
;    APPLICANT:  Rybak, Susanna M.
;    APPLICANT:  Newton, Dianne L.
;    APPLICANT:  Boque, Lluis
;    APPLICANT:  Wlodawer, Alexander
;    TITLE OF INVENTION:  Recombinant Ribonuclease Proteins
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/875,811
;      FILING DATE:  19-FEB-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/02588
;      FILING DATE:  19-FEB-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/011,800
;      FILING DATE:  21-FEB-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faris, Susan K.
;      REGISTRATION NUMBER:  41,739
;      REFERENCE/DOCKET NUMBER:  015280-244100US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  57:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  355 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-875-811-57


  Query Match             73.7%;  Score 501;  DB 3;  Length 355;
  Best Local Similarity   86.4%;  Pred. No. 1.4e-41;
  Matches   95;  Conservative    4;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
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Db     245 GGGSDIQMTQSPSSLSASLGGKVTITCKASQDIKKSIAWYQHKPGKGPRLLIHYTSTLQP 304

Qy      77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           |||||||||||| :|||:|||||||||||||| ||||| |||||||||:|
Db     305 GIPSRFSGSGSGEEYSFSISNLEPEDIATYYCQQYDNLRTFGGGTKLELK 354


Search completed: May  7, 2002, 12:23:03
Job time: 174 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 12:20:29 ; Search time 37.68 Seconds
(without alignments)
254.724 Million cell updates/sec

Title: US-09-155-739-2
Perfect score: 680
Sequence: 1 MRPSIQFLGLLLFWLHGAQC.....YCLQYDNLWTFGGGTKLEIK 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	589	86.6	125	2	S09365	Ig kappa chain - m
2	535	78.7	104	2	S26330	Ig kappa chain V r
3	526	77.4	104	2	S26329	Ig kappa chain V r
4	524	77.1	106	2	C33936	Ig kappa chain V r
5	490.5	72.1	129	2	S52789	Ig kappa chain V r
6	490	72.1	103	2	S26332	Ig light chain V r
7	488	71.8	97	2	PH1064	Ig light chain V r
8	476	70.0	94	2	E33730	Ig kappa chain V r
9	471.5	69.3	107	2	PL0270	Ig kappa chain V r
10	465.5	68.5	107	2	PL0272	Ig kappa chain V r
11	464.5	68.3	107	2	PL0269	Ig kappa chain V r
12	464.5	68.3	107	2	PL0271	Ig kappa chain V r
13	453.5	66.7	127	2	S40367	Ig kappa chain V-J
14	445.5	65.5	132	2	S40334	Ig kappa chain - h
15	444.5	65.4	139	2	S40365	Ig kappa chain - h
16	443.5	65.2	129	2	S40317	Ig kappa chain - h
17	442.5	65.1	125	2	S40333	Ig kappa chain V-J
18	442.5	65.1	131	2	S40352	Ig kappa chain V-J
19	441.5	64.9	129	1	K1HUWK	Ig kappa chain pre
20	439.5	64.6	94	2	PH1063	Ig light chain V r
21	439	64.6	124	2	S40336	Ig kappa chain V-J
22	438.5	64.5	123	2	S40331	Ig kappa chain - h
23	438	64.4	117	2	S42263	Ig kappa chain V r
24	437.5	64.3	122	2	A29380	Ig kappa chain pre
25	437.5	64.3	127	2	S52447	Ig kappa chain V r
26	437.5	64.3	135	2	S24320	Ig kappa chain pre
27	436.5	64.2	128	2	PL0101	Ig kappa chain pre
28	436.5	64.2	129	2	S52793	Ig kappa chain V r
29	435.5	64.0	127	2	S04574	Ig kappa chain pre
30	435.5	64.0	127	2	S11240	Ig kappa chain V r
31	434.5	63.9	141	2	A49134	Ig kappa chain V-I
32	433.5	63.8	126	2	A34904	Ig kappa chain pre
33	433.5	63.8	234	2	S14237	Ig kappa chain pre
34	432	63.5	117	2	S43528	Ig kappa chain V r
35	430.5	63.3	127	2	PH1224	Ig kappa chain pre
36	428.5	63.0	125	2	S40316	Ig kappa chain - h
37	427.5	62.9	129	2	S52792	Ig kappa chain V r
38	426.5	62.7	125	2	S40350	Ig kappa chain - h
39	425.5	62.6	125	2	S40349	Ig kappa chain V-J
40	425.5	62.6	128	1	KVMST1	Ig kappa chain pre
41	422.5	62.1	124	2	S40348	Ig kappa chain V-J
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43	419.5	61.7	124	2	S03521	Ig kappa chain pre
44	418	61.5	127	2	A23986	Ig kappa chain pre
45	416.5	61.2	85	2	F36025	Ig light chain V r

ALIGNMENTS

RESULT 1
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C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S09365
R;Feddersen, R.; van Ness, B.
Nucleic Acids Res. 17, 9797-9809, 1989
A;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene s
A;Reference number: S09365; MUID:90098844
A;Accession: S09365
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <FED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 589; DB 2; Length 125;
Best Local Similarity 90.6%; Pred. No. 4.8e-44;
Matches 115; Conservative 2; Mismatches 6; Indels 4; Gaps 2;

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Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW-TFGG 119
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Db      58 GKGPRLLIHYTSTLQPGIPSRFSGSGSGSDYSFSISNLGPEDIATYYCLQYDNLLRTFGG 117

Qy     120 GTKLEIK 126
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Db     118 GTKLEIK 124
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RESULT 2
S26330
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26330
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26330
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59185; NID:g52316; PIDN:CAA41895.1; PID:g1334063
C;Superfamily: immunoglobulin V region; immunoglobulin homology

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C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>


  Query Match           78.7%;  Score 535;  DB 2;  Length 104;
  Best Local Similarity  95.2%;  Pred. No. 1.8e-39;
  Matches   99;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||||||||||| ||||||:||||||||| ||||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLE 124
           |||||||||||||:|||||||||||||||||||||||||||||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLWTFGGGTKLE 104


RESULT   3
S26329
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26329
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421
A;Accession: S26329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59173; NID:g52309; PIDN:CAA41883.1; PID:g1334059
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>


  Query Match           77.4%;  Score 526;  DB 2;  Length 104;
  Best Local Similarity  94.2%;  Pred. No. 1.1e-38;
  Matches   98;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||||||||||| ||||||:||||||||| ||||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLE 124
           |||||||||||||:|||||||||||||||||||:|||||||||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLE 104


RESULT   4
C33936
Ig kappa chain V region (VM113) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831
A;Accession: C33936
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MEE>
A;Cross-references: GB:J04577; NID:g623187; PIDN:AAA60443.1; PID:g623189
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>


  Query Match           77.1%;  Score 524;  DB 2;  Length 106;
  Best Local Similarity  91.5%;  Pred. No. 1.6e-38;
  Matches   97;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||||||||||| ||||||:||||||||| ||||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYLAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           |||||||||||||:||||:||:||||||||||:|:||||||||||
Db      61 RFSGSGSGRDYSFSISNLDPEEIATYYCLQYDSLYTFGGGTKLEIK 106


RESULT   5
S52789
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Der
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myelo
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>


  Query Match           72.1%;  Score 490.5;  DB 2;  Length 129;
  Best Local Similarity  72.4%;  Pred. No. 1.5e-35;
  Matches   92;  Conservative   15;  Mismatches   19;  Indels    1;  Gaps    1;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           ||   | ||||| || ||:||||||||||||||:| :|||||: ||||: |: ||| ||
Db       3 MRVPAQLLGLLLLWLSGARCDIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKP 62

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
           || |:|||| |:|: |:|||||||||| |:|| ||:|:|||:||||| |||||  ||||
Db      63 GKAPKLLIHAASSLETGVPSRFSGSGSGTDFSFTISSLQPEDLATYYCQQYDNLPLTFGG 122

Qy     120 GTKLEIK 126
           |||:|||
Db     123 GTKVEIK 129


RESULT   6
S26332
Ig light chain V region - mouse (fragment)
N;Alternate names: Ig kappa chain V region
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26332; S26331
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26332
A;Molecule type: mRNA
A;Residues: 1-103 <STA>
A;Cross-references: EMBL:X59187; NID:g52318; PIDN:CAA41897.1; PID:g1334064
A;Note: the sequence of residues 1-8 and the corresponding nucleic acid sequence are
A;Accession: S26331
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <ST2>
A;Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
```

```
  Query Match             72.1%;  Score 490;  DB 2;  Length 103;
  Best Local Similarity   87.4%;  Pred. No. 1.3e-35;
  Matches   90;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||||||| ||| | || :|:|||||||||| |||:: |||:|||||||
Db       1 DIQMTQSPSSLSASLGGKVTFTCKASHDIKRYIAWYQHKPGKGPRLIMDYTSSLQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKL 123
           |||||||||||||:|||||||||||||||||||:||||||||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKL 103


RESULT   7
PH1064
Ig light chain V region (clone 202.54) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1064
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444
A;Accession: PH1064
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>


  Query Match             71.8%;  Score 488;  DB 2;  Length 97;
  Best Local Similarity   93.8%;  Pred. No. 1.9e-35;
  Matches   91;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||||||||||| |||||||:|||||||| |||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTF 117
           |||||||||||||:|||||||||||||||||||:||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLFTF 97


RESULT   8
E33730
Ig kappa chain V region (9.42) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C;Accession: E33730
R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A;Reference number: A33730; MUID:89367325
A;Accession: E33730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <LAW>
A;Cross-references: GB:M26000; NID:g197119; PIDN:AAA38916.1; PID:g197120
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>


  Query Match             70.0%;  Score 476;  DB 2;  Length 94;
  Best Local Similarity   94.7%;  Pred. No. 1.9e-34;
  Matches   89;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||||||||||| |||||||:|||||||| |||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL 114
           |||||||||||||:|||||||||||||||||||||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNL 94


RESULT   9
PL0270
Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0270
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0270
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4


  Query Match             69.3%;  Score 471.5;  DB 2;  Length 107;
  Best Local Similarity   86.0%;  Pred. No. 5.4e-34;
  Matches   92;  Conservative    5;  Mismatches    9;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||| ||||||| ||||||:|||||:| ||||||| || ||||| ||| |||||||
Db       1 DIQMTQSPCSLSASLGDKVTITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           |||||||||||||:|||||||||||||||||||| : :||| |||||||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107


RESULT  10
PL0272
Ig kappa chain V region (anti-DNA, 6B8VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0272
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0272
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4


  Query Match             68.5%;  Score 465.5;  DB 2;  Length 107;
  Best Local Similarity   85.0%;  Pred. No. 1.8e-33;
  Matches   91;  Conservative    5;  Mismatches   10;  Indels    1;  Gaps    1;
```

```
Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||| ||||||| || |||:|||||:| ||||||| || ||||| ||| |||||||
Db       1 DIQMTQSPCSLSASLGDKVIITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           |||||||||||||:|||||||||||||||||| : :||| |||||||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107


RESULT  11
PL0269
Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0269
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0269
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4


  Query Match             68.3%;  Score 464.5;  DB 2;  Length 107;
  Best Local Similarity   85.0%;  Pred. No. 2.2e-33;
  Matches   91;  Conservative    4;  Mismatches   11;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||| || | |:||||| | ||||||| || ||||| ||| |||||||
Db       1 DIQMTQSPSSLSASLGDKVIIACRTSQDIRKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           |||||||||||||:|||||||||||||||||| : :||| |||||||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107


RESULT  12
PL0271
Ig kappa chain V region (anti-DNA, 2E3VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0271
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0271
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4


  Query Match             68.3%;  Score 464.5;  DB 2;  Length 107;
  Best Local Similarity   85.0%;  Pred. No. 2.2e-33;
  Matches   91;  Conservative    4;  Mismatches   11;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||| ||||||| || |||:|||||:| ||||||| || ||||| ||| |||||||
Db       1 DIQMTQSPCSLSASLGDKVIITCRTSQDIRKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           |||||||||||||:|||||||||||||||||| : :||| |||||||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107


RESULT  13
S40367
Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40367
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40367
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-127 <KLE>
A;Cross-references: EMBL:X72477
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>


  Query Match             66.7%;  Score 453.5;  DB 2;  Length 127;
  Best Local Similarity   68.9%;  Pred. No. 2.3e-32;
  Matches   84;  Conservative   16;  Mismatches   21;  Indels    1;  Gaps    1;

Qy       6 QFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPR 65
           | ||||| || ||:|||||||||||||||:| :|||||: || |: |: ||| |||| |:
Db       3 QLLGLLLLWLRGARCDIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQRKPGKAPK 62

Qy      66 LLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLE 124
           |||:  |:|| |:|||||||||| |::  ||:|:||| ||||| | |:  |||| |||:|
Db      63 LLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYNTPWTFGQGTKVE 122

Qy     125 IK 126
           ||
Db     123 IK 124


RESULT  14
S40334
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40334
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40334
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-132 <KLE>
A;Cross-references: EMBL:X72444
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;37-111/Domain: immunoglobulin homology <IMM>


  Query Match             65.5%;  Score 445.5;  DB 2;  Length 132;
  Best Local Similarity   64.6%;  Pred. No. 1.1e-31;
  Matches   82;  Conservative   21;  Mismatches   23;  Indels    1;  Gaps    1;
```

```
Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           ||   | ||||| || ||:||||:|||||  ||||:| :|||||: || || |:|||| ||
Db       2 MRVPAQLLGLLLLWLPGARCDIQLTQSPSFLSASIGDRVTITCRASQGINSYLAWYQQKP 61

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
           || |:|||:  | || |:||||||||||| :::  ||:|:||| |:||| |::  :|||| 
Db      62 GKAPKLLIYVASTLQSGVPSRFSGSGSGTEFTLTISSLQPEDFASYYCQQFNSYPFTFGG 121

Qy     120 GTKLEIK 126
           |||:||:
Db     122 GTKVEIR 128


RESULT  15
S40365
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40365
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891
A;Accession: S40365
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-139 <KLE>
A;Cross-references: EMBL:X72475; NID:g441418; PIDN:CAA51143.1; PID:g441419
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>


  Query Match             65.4%;  Score 444.5;  DB 2;  Length 139;
  Best Local Similarity   68.9%;  Pred. No. 1.5e-31;
  Matches   84;  Conservative   14;  Mismatches   23;  Indels    1;  Gaps    1;

Qy       6 QFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPR 65
           | ||||| || || ||||||||||||||||:| :|||||: :|||  |: |||||||| |
Db       1 QLLGLLLLWLSGATCDIQMTQSPSSLSASVGDRVTITCQATQDIGNYLNWYQHKPGKAPN 60

Qy      66 LLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLE 124
           |||:  | |: |:|||||| |||  ::| ||:|:|||||||||| || || :||| |||: 
Db      61 LLIYDASNLETGVPSRFSGRGSGTHFTFTISSLQPEDIATYYCQQYGNLPFTFGPGTKVH 120

Qy     125 IK 126
           ||
Db     121 IK 122


Search completed: May  7, 2002, 12:23:47
Job time: 198 sec
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:23:09 ; Search time 21.92 Seconds
(without alignments)
210.756 Million cell updates/sec

Title: US-09-155-739-2
Perfect score: 680
Sequence: 1 MRPSIQFLGLLLFWLHGAQC.....YCLQYDNLWTFGGGTKLEIK 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	441.5	64.9	129	1	KV1W_HUMAN	P04431 homo sapien
2	425.5	62.6	128	1	KV5E_MOUSE	P01637 mus musculu
3	412.5	60.7	129	1	KV1X_HUMAN	P04432 homo sapien
4	402	59.1	117	1	KV1J_HUMAN	P01602 homo sapien
5	400	58.8	115	1	KV5F_MOUSE	P01638 mus musculu
6	397.5	58.5	108	1	KV1B_HUMAN	P01594 homo sapien
7	395.5	58.2	108	1	KV1O_HUMAN	P01607 homo sapien
8	392.5	57.7	108	1	KV1P_HUMAN	P01608 homo sapien
9	389.5	57.3	108	1	KV1Y_HUMAN	P80362 homo sapien
10	380.5	56.0	108	1	KV1A_HUMAN	P01593 homo sapien
11	379.5	55.8	108	1	KV1M_HUMAN	P01605 homo sapien
12	378.5	55.7	130	1	KV5G_MOUSE	P01639 mus musculu
13	378.5	55.7	133	1	KV4B_HUMAN	P06313 homo sapien
14	378	55.6	117	1	KV1I_HUMAN	P01601 homo sapien
15	377.5	55.5	108	1	KV5J_MOUSE	P01643 mus musculu
16	377	55.4	107	1	KV1D_HUMAN	P01596 homo sapien
17	375	55.1	134	1	KV4C_HUMAN	P06314 homo sapien
18	374.5	55.1	108	1	KV5O_MOUSE	P01648 mus musculu
19	373.5	54.9	108	1	KV1Q_HUMAN	P01609 homo sapien
20	373.5	54.9	108	1	KV5N_MOUSE	P01647 mus musculu
21	371.5	54.6	108	1	KV5K_MOUSE	P01644 mus musculu
22	369.5	54.3	108	1	KV5M_MOUSE	P01646 mus musculu
23	368.5	54.2	108	1	KV5L_MOUSE	P01645 mus musculu
24	366.5	53.9	108	1	KV1R_HUMAN	P01610 homo sapien
25	362.5	53.3	108	1	KV1C_HUMAN	P01595 homo sapien
26	360.5	53.0	108	1	KV1H_HUMAN	P01600 homo sapien
27	359.5	52.9	108	1	KV1N_HUMAN	P01606 homo sapien
28	357.5	52.6	108	1	KV1E_HUMAN	P01597 homo sapien
29	357.5	52.6	108	1	KV1V_HUMAN	P04430 homo sapien
30	355.5	52.3	108	1	KV1F_HUMAN	P01598 homo sapien
31	354.5	52.1	108	1	KV1S_HUMAN	P01611 homo sapien
32	353.5	52.0	115	1	KV5C_MOUSE	P01635 mus musculu
33	352.5	51.8	108	1	KV1K_HUMAN	P01603 homo sapien
34	350.5	51.5	108	1	KV1L_HUMAN	P01604 homo sapien
35	349.5	51.4	108	1	KV5U_MOUSE	P04946 mus musculu
36	347	51.0	129	1	KV3H_HUMAN	P04207 homo sapien
37	347	51.0	129	1	KV3M_HUMAN	P18136 homo sapien
38	343	50.4	117	1	KV5H_MOUSE	P01641 mus musculu
39	341.5	50.2	108	1	KV1G_HUMAN	P01599 homo sapien
40	341	50.1	110	1	KV3P_MOUSE	P01668 mus musculu
41	339.5	49.9	108	1	KV5T_MOUSE	P01653 mus musculu
42	338	49.7	129	1	KV3L_HUMAN	P18135 homo sapien
43	337.5	49.6	131	1	KV3I_MOUSE	P01661 mus musculu
44	335.5	49.3	108	1	KV5P_MOUSE	P01649 mus musculu
45	335.5	49.3	108	1	KV5Q_MOUSE	P01650 mus musculu

ALIGNMENTS

```
RESULT 1
KV1W_HUMAN
ID   KV1W_HUMAN     STANDARD;      PRT;   129 AA.
AC   P04431;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X00965; CAA25477.1; ALT_TERM.
DR   PIR; A01883; K1HUWK.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       IG KAPPA CHAIN V-I REGION WALKER.
FT   DOMAIN       23     45       FRAMEWORK 1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       57     71       FRAMEWORK 2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       79    110       FRAMEWORK 3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      120    129       FRAMEWORK 4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14069 MW;  F941FA07D4AFC2F9 CRC64;


  Query Match             64.9%;  Score 441.5;  DB 1;  Length 129;
  Best Local Similarity   66.9%;  Pred. No. 5.2e-38;
  Matches   85;  Conservative   15;  Mismatches   26;  Indels    1;  Gaps    1;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           ||    | ||||| || ||:||||||||||||||||:| :||||||: || |: |: ||| ||
```

```
Db       3 MRVPAQLLGLLLLWLRGARCDIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKP 62

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
           || |:|||:  |:|| |: |||||||| |::  ||:|:||| ||||| | |  | |||
Db      63 GKAPKLLIYAASSLQSGVTSRFSGSGSGTDFTLTISSLQPEDSATYYCQQSYSTLITFGQ 122

Qy     120 GTKLEIK 126
           |||:||||
Db     123 GTRLEIK 129


RESULT   2
KV5E_MOUSE
ID   KV5E_MOUSE     STANDARD;      PRT;   128 AA.
AC   P01637;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-V REGION T1 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81052342; PubMed=6776411;
RA   Altenburger W., Steinmetz M., Zachau H.G.;
RT   "Functional and non-functional joining in immunoglobulin light chain
RT   genes of a mouse myeloma.";
RL   Nature 287:603-607(1980).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; V00772; CAA24150.1; -.
DR   PIR; A01920; KVMST1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    128       IG KAPPA CHAIN V-V REGION T1.
FT   DOMAIN       21     43       FRAMEWORK 1.
FT   DOMAIN       44     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     69       FRAMEWORK 2.
FT   DOMAIN       70     76       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       77    108       FRAMEWORK 3.
FT   DOMAIN      109    117       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      118    127       FRAMEWORK 4.
FT   DISULFID     43    108       BY SIMILARITY.
FT   NON_TER     128    128
SQ   SEQUENCE   128 AA;  14385 MW;  AFA5563D31BB7E05 CRC64;


  Query Match             62.6%;  Score 425.5;  DB 1;  Length 128;
  Best Local Similarity   62.2%;  Pred. No. 2.2e-36;
  Matches   79;  Conservative   18;  Mismatches   29;  Indels    1;  Gaps    1;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           ||   ||||:|| |  | :|||:||||||: |||| :|||:|| ||||| |: |:| ||
Db       1 MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVTISCKASQDINSYLTWFQQKP 60

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGG 119
           || |: |::  : |  |:||||||||||:|:|  ||:|| ||:  ||||||     |||
Db      61 GKSPKTLLYRANRLVDGVPSRFSGSGSGQDFSLTISSLEYEDMGIYYCLQYDEFPLTFGA 120

Qy     120 GTKLEIK 126
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           |||||:|
Db     121 GTKLELK 127


RESULT   3
KV1X_HUMAN
ID   KV1X_HUMAN     STANDARD;      PRT;   129 AA.
AC   P04432;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION DAUDI PRECURSOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X00966; CAA25478.1; ALT_TERM.
DR   PIR; A01884; K1HUDI.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       IG KAPPA CHAIN V-I REGION DAUDI.
FT   DOMAIN       23     45       FRAMEWORK 1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       57     71       FRAMEWORK 2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       79    110       FRAMEWORK 3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      120    129       FRAMEWORK 4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14235 MW;  CAF076BC7E5574C8 CRC64;


  Query Match             60.7%;  Score 412.5;  DB 1;  Length 129;
  Best Local Similarity   61.4%;  Pred. No. 4.5e-35;
  Matches   78;  Conservative   19;  Mismatches   29;  Indels    1;  Gaps    1;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           ||   | ||||| ||   :|||||||||||||||:| :|||||:   :|  :::||| ||
Db       3 MRVPAQLLGLLLLWLRRVRCDIQMTQSPSSLSASVGDRVTITCRAGHNITNFLSWYQQKP 62

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGG 119
           || | |||:  | || |:|||||||||| ::::  ||:|:||| ||||| | |:  :||||
Db      63 GKAPTLLIYAVSNLQVGVPSRFSGSGSGAEFTLTISSLQPEDFATYYCQQNYNFSFTFGG 122

Qy     120 GTKLEIK 126
           |||:: |
Db     123 GTKVDNK 129


RESULT   4
KV1J_HUMAN
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ID   KV1J_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01602;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION HK102 PRECURSOR (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81098966; PubMed=6779204;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Human immunoglobulin variable region genes -- DNA sequences of two V
RT   kappa genes and a pseudogene.";
RL   Nature 288:730-733(1980).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00245; AAA59087.1; -.
DR   EMBL; Z00001; CAA77292.1; -.
DR   PIR; A01882; K1HU12.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23   >117       IG KAPPA CHAIN V-I REGION HK102.
FT   DOMAIN       23     45       FRAMEWORK 1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       57     71       FRAMEWORK 2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       79    110       FRAMEWORK 3.
FT   DOMAIN      111   >117       COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12768 MW;  AD1DF3A40AF1A49B CRC64;


  Query Match             59.1%;  Score 402;  DB 1;  Length 117;
  Best Local Similarity   63.7%;  Pred. No. 4.7e-34;
  Matches   72;  Conservative   21;  Mismatches   20;  Indels    0;  Gaps    0;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           ||   | ||||| || ||:||||||||||:||||:| :|||||: || |: ::|||| ||
Db       3 MRVPAQLLGLLLLWLPGAKCDIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKP 62

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN 113
           || |:|||:  |:|: |:|||||||||| ::::  ||:|:|:| ||||| ||::
Db      63 GKAPKLLIYDASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNS 115


RESULT   5
KV5F_MOUSE
ID   KV5F_MOUSE     STANDARD;      PRT;   115 AA.
AC   P01638;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-V REGION L6 PRECURSOR (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81220975; PubMed=6264318;
RA   Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT   "Differences between germ-line and rearranged immunoglobulin V kappa
RT   coding sequences suggest a localized mutation mechanism.";
RL   Nature 291:668-670(1981).
DR   PIR; A01921; KVMSL6.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21   >115       IG KAPPA CHAIN V-V REGION L6.
FT   DOMAIN       21     43       FRAMEWORK 1.
FT   DOMAIN       44     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     69       FRAMEWORK 2.
FT   DOMAIN       70     76       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       77    108       FRAMEWORK 3.
FT   DOMAIN      109   >115       COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID     43    108       BY SIMILARITY.
FT   NON_TER     115    115
SQ   SEQUENCE   115 AA;  12986 MW;  BA852C58F328E1C3 CRC64;


  Query Match             58.8%;  Score 400;  DB 1;  Length 115;
  Best Local Similarity   65.2%;  Pred. No. 7.4e-34;
  Matches   73;  Conservative   15;  Mismatches   24;  Indels    0;  Gaps    0;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           ||   ||||:|| |  | :|||:||||||: |||| :|||||| ||||| |::|:| ||
Db       1 MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKP 60

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYD 112
           || |: ||:  : |  |:||||||||||:|||  ||:|| ||:  |||||||
Db      61 GKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQYD 112


RESULT   6
KV1B_HUMAN
ID   KV1B_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the
RT   Bence-Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC       MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC       REGION OF THE KAPPA CHAIN REI.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01862; K1HUAU.
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DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11939 MW;  E8011187EE6F6FB9 CRC64;


  Query Match             58.5%;  Score 397.5;  DB 1;  Length 108;
  Best Local Similarity   70.1%;  Pred. No. 1.2e-33;
  Matches   75;  Conservative   14;  Mismatches   17;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||:| :|||||: |||| |: ||| |||| |:|||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           |||| |||  ::| ||:|:|||||||| ||| | |||| |||:|||
Db      61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK 107


RESULT   7
KV1O_HUMAN
ID   KV1O_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION REI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei.); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01873; K1HURE.
DR   PDB; 1REI; 17-FEB-84.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       85     90
FT   STRAND       98     98
FT   STRAND      102    106
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;


  Query Match             58.2%;  Score 395.5;  DB 1;  Length 108;
  Best Local Similarity   71.7%;  Pred. No. 2e-33;
  Matches   76;  Conservative   13;  Mismatches   16;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||:| :|||||: |||| ||: |||  ||| |:|||:  | || |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEI 125
           |||||||| ||:| ||:|:|||||||||| || :| :||| ||||:|
Db      61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106


RESULT   8
KV1P_HUMAN
ID   KV1P_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01608;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION ROY.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=68362076; PubMed=5595110;
RA   Hilschmann N.;
RT   "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT   Cum.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN   [2]
RP   REVISIONS TO 39 AND 41.
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RL   (In) Franek F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press,
RL   New York (1969).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01874; K1HURY.
DR   HSSP; P80362; 1WTL.
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DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11782 MW;  F5ACEDE5A313DF3A CRC64;


  Query Match             57.7%;  Score 392.5;  DB 1;  Length 108;
  Best Local Similarity   68.2%;  Pred. No. 4e-33;
  Matches   73;  Conservative   18;  Mismatches   15;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||:| :|||||: |||| :: ||| |||| |:|||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDISIFLNWYQQKPGKAPKLLIYDASKLEAGVPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           ||||:||| |::| ||:|:|||||||| |:||| |||||||:: |
Db      61 RFSGTGSGTDFTFTISSLQPEDIATYYCQQFDNLPLTFGGGTKVDFK 107


RESULT   9
KV1Y_HUMAN
ID   KV1Y_HUMAN     STANDARD;      PRT;   108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=95086080; PubMed=7993911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
RN   [2]
RP   SEQUENCE OF 1-35.
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human kI Bence Jones protein Wat.";
RL   J. Mol. Biol. 147:185-193(1981).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PDB; 1WTL; 01-NOV-94.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   CONFLICT     30     31       TN -> SD (IN REF. 2).
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11737 MW;  D9D941B3F0FAE697 CRC64;


  Query Match             57.3%;  Score 389.5;  DB 1;  Length 108;
  Best Local Similarity   67.3%;  Pred. No. 8e-33;
  Matches   72;  Conservative   18;  Mismatches   16;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||:| :|||||: |||| |: |:| :||: |::||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           |||||||| |::| ||:|:|||||||| ||| |  |||||||::||
Db      61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDTLPLTFGGGTKVDIK 107


RESULT  10
KV1A_HUMAN
ID   KV1A_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01593;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION AG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69234734; PubMed=4893682;
RA   Titani K., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT   complete sequence and the location of the disulfide bridges.";
RL   J. Biol. Chem. 244:3550-3560(1969).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01861; K1HUAG.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11992 MW;  E3B3B246C18F0C4F CRC64;


  Query Match             56.0%;  Score 380.5;  DB 1;  Length 108;
  Best Local Similarity   69.2%;  Pred. No. 6.5e-32;
  Matches   74;  Conservative   12;  Mismatches   20;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||:| :|||||: ||||| |: |||  | | |::||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDINHYLNWYQQGPKKAPKILIYDASNLETGVPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           ||||||  | |::| || |:|||||||| ||| |  ||| |||||||
Db      61 RFSGSGFGTDFTFTISGLQPEDIATYYCQQYDTLPRTFGQGTKLEIK 107


RESULT  11
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KV1M_HUMAN
ID   KV1M_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01605;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION LAY.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77038198; PubMed=824717;
RA   Capra J.D., Klapper D.G.;
RT   "Complete amino acid sequence of the variable domains of two human
RT   IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT   specificities.";
RL   Scand. J. Immunol. 5:677-684(1976).
CC   -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC       CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC       WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC       GLOBULIN ACTIVITY.
DR   PIR; A01871; K1HULY.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  739993A95431434A CRC64;
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  Query Match             55.8%;  Score 379.5;  DB 1;  Length 108;
  Best Local Similarity   65.7%;  Pred. No. 8.2e-32;
  Matches   71;  Conservative   17;  Mismatches   17;  Indels    3;  Gaps    2;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||| |:| :|||||: ||::| |: ||| |||  |:|||: |  : |:||
Db       1 DIQMTQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW--TFGGGTKLEIK 126
           |||||||| |::| ||:|:|||||||||| ||:| |  ||| |||:|:|
Db      61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYNN-WPPTFGQGTKVEVK 107
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RESULT  12
KV5G_MOUSE
ID   KV5G_MOUSE     STANDARD;      PRT;   130 AA.
AC   P01639; P01640;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-V REGION MOPC 41 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=79221900; PubMed=111146;
RA   Seidman J.G., Max E.E., Leder P.;
RT   "A kappa immunoglobulin gene is formed by site-specific recombination
RT   without further somatic mutation.";
RL   Nature 280:370-375(1979).
RN   [2]
RP   SEQUENCE OF 1-33.
RX   MEDLINE=77148916; PubMed=403522;
RA   Burstein Y., Schechter I.;
RT   "Amino acid sequence of the NH2-terminal extra piece segments of the
RT   precursors of mouse immunoglobulin lambdal-type and kappa-type light
RT   chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
RN   [3]
RP   SEQUENCE OF 23-130.
RX   MEDLINE=67056897; PubMed=4162931;
RA   Gray W.R., Dreyer W.J., Hood L.;
RT   "Mechanism of antibody synthesis: size differences between mouse
RT   kappa chains.";
RL   Science 155:465-467(1967).
CC   -!- MISCELLANEOUS: THIS PRECURSOR WAS SYNTHESIZED IN A CELL-FREE
CC       SYSTEM DIRECTED BY MRNA ISOLATED FROM MYELOMA POLYSOMES.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01922; KVMSM4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal; Bence-Jones protein.
FT   SIGNAL        1     22
FT   CHAIN        23    130       IG KAPPA CHAIN V-V REGION MOPC 41.
FT   DOMAIN       23     45       FRAMEWORK 1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       57     71       FRAMEWORK 2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       79    110       FRAMEWORK 3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      120    129       FRAMEWORK 4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   VARIANT       1      2       MISSING (IN 25% OF THE MOLECULES).
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  14311 MW;  5EFE0FE71D5F1BEC CRC64;
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  Query Match             55.7%;  Score 378.5;  DB 1;  Length 130;
  Best Local Similarity   59.1%;  Pred. No. 1.3e-31;
  Matches   75;  Conservative   13;  Mismatches   38;  Indels    1;  Gaps    1;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           ||    |  | ||    | :|||||||||||||||| :|::||: ||||   : | | :|
Db       3 MRAPAQIFGFLLLLFQGTRCDIQMTQSPSSLSASLGERVSLTCRASQDIGSSLNWLQQEP 62

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGG 119
           : ||: ||:|  |:| ||||| || |||  ||:|| ||   |||||  : |||||
Db      63 DGTIKRLIYATSSLDSGVPKRFSGSRSGSDYSLTISSLESEDFVDYYCLQYASSPWTFGG 122

Qy     120 GTKLEIK 126
           |||||||
Db     123 GTKLEIK 129
```

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RESULT  13
KV4B_HUMAN
ID   KV4B_HUMAN     STANDARD;      PRT;   133 AA.
AC   P06313;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-IV REGION JI PRECURSOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86041853; PubMed=2997712;
```

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RA   Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA   Zachau H.G.;
RT   "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT   single germline gene.";
RL   Nucleic Acids Res. 13:6515-6529(1985).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z00022; CAA77317.1; -.
DR   PIR; A01904; K4HUJI.
DR   HSSP; P01789; 2MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    133       IG KAPPA CHAIN V-IV REGION JI.
FT   DOMAIN       21     43       FRAMEWORK 1.
FT   DOMAIN       44     60       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       61     75       FRAMEWORK 2.
FT   DOMAIN       76     82       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       83    114       FRAMEWORK 3.
FT   DOMAIN      115    122       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      123    132       FRAMEWORK 4.
FT   DISULFID     43    114       BY SIMILARITY.
FT   NON_TER     133    133
SQ   SEQUENCE   133 AA;  14632 MW;  5FB3953066744AF4 CRC64;
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  Query Match             55.7%;  Score 378.5;  DB 1;  Length 133;
  Best Local Similarity   57.9%;  Pred. No. 1.3e-31;
  Matches   73;  Conservative   20;  Mismatches   26;  Indels    7;  Gaps    3;

Qy       7 FLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDI-----NK-YMAWYQHKP 60
           |: ||| |: ||  || ||||| ||: ||| : || ||:|| :     || |:|||| ||
Db       8 FISLLL-WISGAYGDIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKP 66

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGG 120
             |: |:|||:: |  : |:| |||||||| |::  ||:|: ||:| ||| ||| : |||||
Db      67 GQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYDTIPTFGGG 126

Qy     121 TKLEIK 126
           ||:|||
Db     127 TKVEIK 132
```

```
RESULT  14
KV1I_HUMAN
ID   KV1I_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01601;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION HK101 PRECURSOR (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81098966; PubMed=6779204;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Human immunoglobulin variable region genes -- DNA sequences of two V
RT   kappa genes and a pseudogene.";
RL   Nature 288:730-733(1980).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83129397; PubMed=6402305;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Evolution of immunoglobulin V genes: evidence indicating that
RT   recently duplicated human V kappa sequences have diverged by gene
RT   conversion.";
RL   Cell 32:181-189(1983).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; K01322; AAA58930.1; -.
DR   EMBL; K01324; AAA58932.1; -.
DR   EMBL; V00558; CAA23824.1; -.
DR   PIR; A01881; K1HU11.
DR   PIR; A21056; A21056.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23   >117       IG KAPPA CHAIN V-I REGION HK101.
FT   DOMAIN       23     45       FRAMEWORK 1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       57     71       FRAMEWORK 2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       79    110       FRAMEWORK 3.
FT   DOMAIN      111   >117       COMPLEMENTARITY-DETERMINING 3.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12799 MW;  D7D0FF3718CEF587 CRC64;
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  Query Match             55.6%;  Score 378;  DB 1;  Length 117;
  Best Local Similarity   62.8%;  Pred. No. 1.3e-31;
  Matches   71;  Conservative   17;  Mismatches   25;  Indels    0;  Gaps    0;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKP 60
           ||   | |||||    ||:|||||||||||||||:| :|||||:  | |: ::|||| ||
Db       3 MRVLAQLLGLLLLCFPGARCDIQMTQSPSSLSASVGDRVTITCRARQGISSWLAWYQQKP 62

Qy      61 GKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDN 113
             | |: ||:  |:|| |:||||||||||| |::  ||:|:|||| ||||| ||::
Db      63 EKAPKSLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNS 115
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RESULT  15
KV5J_MOUSE
ID   KV5J_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01643;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-V REGION MOPC 173.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76091934; PubMed=812696;
RA   Schiff C., Fougereau M.;
RT   "Determination of the primary structure of a mouse IgG2a
RT   immunoglobulin. Amino-acid sequence of the light chain.";
RL   Eur. J. Biochem. 59:525-537(1975).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
```

```
DR   PIR; A01926; KVMS73.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    108       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11819 MW;  2AD29D92A72AA0A3 CRC64;


  Query Match             55.5%;  Score 377.5;  DB 1;  Length 108;
  Best Local Similarity   67.3%;  Pred. No. 1.3e-31;
  Matches   72;  Conservative   12;  Mismatches   22;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           ||||||: |||||||| :|||:|  || |  |: ||| ||    :|||:|||:|  |:||
Db       1 DIQMTQTTSSLSASLGDRVTISCSASQSIGNYLBWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           |||||||| |||  ||:|:|::|||||| ||  |  ||||||||||
Db      61 RFSGSGSGTDYSLTISBLZPZBIATYYCQQYSKLPRTFGGGTKLEIK 107


Search completed: May  7, 2002, 12:32:34
Job time: 565 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:21:14 ; Search time 67.26 Seconds
(without alignments)
274.016 Million cell updates/sec

Title: US-09-155-739-2
Perfect score: 680
Sequence: 1 MRPSIQFLGLLLFWLHGAQC.....YCLQYDNLWTFGGGTKLEIK 126

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	389.5	57.3	108	4	Q9UL77	Q9ul77 homo sapien
2	380.5	56.0	214	11	Q9R1A5	Q9r1a5 mus musculu
3	378.5	55.7	108	4	Q9UL70	Q9ul70 homo sapien
4	372.5	54.8	107	11	Q9JL84	Q9jl84 mus musculu
5	362	53.2	107	4	Q9UL81	Q9ul81 homo sapien
6	346.5	51.0	108	4	Q9UL79	Q9ul79 homo sapien
7	341.5	50.2	298	11	Q9QYF0	Q9qyf0 mus musculu
8	319	46.9	109	4	Q9UL78	Q9ul78 homo sapien
9	317.5	46.7	238	11	Q99M37	Q99m37 mus musculu
10	310	45.6	109	4	Q9UL85	Q9ul85 homo sapien
11	308	45.3	109	4	Q9UL86	Q9ul86 homo sapien
12	305.5	44.9	108	4	Q9UL83	Q9ul83 homo sapien
13	299	44.0	106	5	Q9U410	Q9u410 schistosoma
14	295.5	43.5	107	11	Q9ERZ9	Q9erz9 mus musculu
15	292.5	43.0	101	11	Q9JL78	Q9jl78 mus musculu
16	291.5	42.9	97	11	Q9JL76	Q9jl76 mus musculu
17	289.5	42.6	103	11	Q9JL80	Q9jl80 mus musculu
18	288.5	42.4	99	11	Q9JL74	Q9jl74 mus musculu
19	281.5	41.4	114	4	Q9UL80	Q9ul80 homo sapien
20	262	38.5	104	11	Q9JL82	Q9jl82 mus musculu
21	252.5	37.1	109	6	Q9N0W5	Q9n0w5 oryctolagus
22	209	30.7	107	4	Q9NSD6	Q9nsd6 homo sapien
23	204.5	30.1	107	4	Q9UL82	Q9ul82 homo sapien
24	193.5	28.5	130	4	Q9NP29	Q9np29 homo sapien
25	188.5	27.7	235	11	Q99M11	Q99m11 mus musculu
26	185	27.2	109	11	Q9ET13	Q9et13 mus musculu
27	150	22.1	337	13	Q9IB02	Q9ib02 sphoeroides
28	140.5	20.7	93	4	Q9UL76	Q9ul76 homo sapien
29	140	20.6	135	4	Q9H5Z4	Q9h5z4 homo sapien
30	129	19.0	100	6	O77624	O77624 bos taurus
31	124	18.2	169	4	Q9Y2N4	Q9y2n4 homo sapien
32	119	17.5	509	11	Q9QWI5	Q9qwi5 rattus norv
33	119	17.5	509	11	P97710	P97710 rattus norv
34	118.5	17.4	342	13	Q9IB00	Q9ib00 sphoeroides
35	117	17.2	509	11	Q9QX57	Q9qx57 mus musculu
36	117	17.2	513	11	P97797	P97797 mus musculu
37	116	17.1	418	11	O70426	O70426 rattus norv
38	115.5	17.0	503	4	P78324	P78324 homo sapien
39	115	16.9	487	11	Q99KA4	Q99ka4 mus musculu
40	115	16.9	509	11	O08907	O08907 mus musculu
41	113.5	16.7	334	13	Q9IB05	Q9ib05 sphoeroides
42	111.5	16.4	361	4	Q9H1U5	Q9h1u5 homo sapien
43	110.5	16.2	372	4	Q9Y4V0	Q9y4v0 homo sapien
44	110.5	16.2	473	11	Q9D8L4	Q9d8l4 mus musculu
45	110	16.2	123	11	Q61243	Q61243 mus musculu

ALIGNMENTS

```
RESULT 1
Q9UL77
ID   Q9UL77      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035037; AAD56273.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11738 MW;  C06681716C4D16F3 CRC64;

  Query Match             57.3%;  Score 389.5;  DB 4;  Length 108;
  Best Local Similarity   68.2%;  Pred. No. 5.6e-35;
  Matches   73;  Conservative   13;  Mismatches   20;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           ||||||||||||||:| :|||||: || |: |: ||| |||| | |||:  |:|| |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKLEIK 126
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          |||||||| |::  ||:|:||| ||||| | |   |||| |||:|||
Db      61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK 107


RESULT   2
Q9R1A5
ID   Q9R1A5      PRELIMINARY;      PRT;   214 AA.
AC   Q9R1A5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab 7, its light and heavy chains) and construction of a
RT   single chain antibody (scFV).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF152371; AAD40242.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     214    214
SQ   SEQUENCE   214 AA;  23922 MW;  52BA205FDE995E2A CRC64;


  Query Match             56.0%;  Score 380.5;  DB 11;  Length 214;
  Best Local Similarity   67.3%;  Pred. No. 1.2e-33;
  Matches   72;  Conservative   14;  Mismatches   20;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||:|||||: |||| :|||||| ||||| |::|:| |||| |: ||:  : |  |:||
Db       1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           ||||||||:||| ||:|| ||:  ||||||| :||| |||||||
Db      61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEIK 107


RESULT   3
Q9UL70
ID   Q9UL70      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035044; AAD56280.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11633 MW;  B7BEDC3E41FCCA37 CRC64;


  Query Match             55.7%;  Score 378.5;  DB 4;  Length 108;
  Best Local Similarity   67.3%;  Pred. No. 8.9e-34;
  Matches   72;  Conservative   16;  Mismatches   18;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||:| :|||||: || |: |:|||| |||| |: ||:  | || |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           |||||||| |::  ||:|:|||:||||| :|::   ||| |||||||
Db      61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107


RESULT   4
Q9JL84
ID   Q9JL84      PRELIMINARY;      PRT;   107 AA.
AC   Q9JL84;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206022; AAF69320.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11648 MW;  ACF9B1253ACA1E5D CRC64;


  Query Match             54.8%;  Score 372.5;  DB 11;  Length 107;
  Best Local Similarity   68.2%;  Pred. No. 4e-33;
  Matches   73;  Conservative    7;  Mismatches   26;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           ||||||| |||||||| :|   |  || |:  |:| ||    :|||:|||:|  |:||
Db       1 DIQMTQSTSSLSASLGDRVXXXCSASQGISNXXXWFQQKPDGTVKLLIYYTSSLXSGVPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           |||||||| |||  |||||||||||||| ||    ||||||||||||
Db      61 RFSGSGSGXDYSLTISNLEPEDIATYYCQQYSKFPWTFGGGTKLEIK 107


RESULT   5
Q9UL81
ID   Q9UL81      PRELIMINARY;      PRT;   107 AA.
AC   Q9UL81;
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DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035033; AAD56269.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11501 MW;  070549FDE0754748 CRC64;


  Query Match             53.2%;  Score 362;  DB 4;  Length 107;
  Best Local Similarity   64.2%;  Pred. No. 5.5e-32;
  Matches   68;  Conservative   15;  Mismatches   23;  Indels    0;  Gaps    0;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           |||||||||||||||:| :|||||: || |: |: ||| |||| | |||:  |:|| |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
           ||||||||  |::  || |: || ||||| |   :  ||| |||::|:
Db      61 RFSGSGSGTDFTLTISGLQAEDFATYYCQQSYSALTFGPGTKVDIR 106


RESULT   6
Q9UL79
ID   Q9UL79      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035035; AAD56271.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11787 MW;  DB5845F19724FB4E CRC64;


  Query Match             51.0%;  Score 346.5;  DB 4;  Length 108;
  Best Local Similarity   64.5%;  Pred. No. 2.7e-30;
  Matches   69;  Conservative   12;  Mismatches   25;  Indels    1;  Gaps    1;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           || |||||| |||| | :|||:|: || |: |:|||| |||| | |||:  | || |:||
Db       1 DIVMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAASTLQSGVPS 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           |||||||| |::  || |: || ||||| || :   ||| |||:|||
Db      61 RFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFPPTFGQGTKVEIK 107


RESULT   7
Q9QYF0
ID   Q9QYF0      PRELIMINARY;      PRT;   298 AA.
AC   Q9QYF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CN 8 SCFV.
GN   CN 8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=SPLEEN;
RA   Shinohara N., Demura T., Fukuda H.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=SPLEEN;
RA   shinohara N., Demura T., Fukuda H.;
RT   "Isolation of a novel type of vascular cell wall-specific monoclonal
RT   antibody recognizing a cell polarity using a phage display subtraction
RT   method.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AB036341; BAA88633.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 2.
SQ   SEQUENCE   298 AA;  31867 MW;  E0F96B8A17004317 CRC64;


  Query Match             50.2%;  Score 341.5;  DB 11;  Length 298;
  Best Local Similarity   57.7%;  Pred. No. 3e-29;
  Matches   64;  Conservative   18;  Mismatches   28;  Indels    1;  Gaps    1;

Qy      17 GAQCDIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQP 76
           |   ||::||||:|||||:|  |||||: | :|: |:|||| | || |:||::    |
Db     169 GGGSDIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLAD 228

Qy      77 GIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGGGTKLEIK 126
           |:|||||||||  ||  |::|:|||  :|||  :    :||||||||||
Db     229 GVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK 279


RESULT   8
Q9UL78
ID   Q9UL78      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
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OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035036; AAD56272.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11646 MW;  5F675C52EC7EE197 CRC64;

  Query Match             46.9%;  Score 319;  DB 4;  Length 109;
  Best Local Similarity   57.4%;  Pred. No. 2.7e-27;
  Matches   62;  Conservative   17;  Mismatches   27;  Indels    2;  Gaps    2;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDI-NKYMAWYQHKPGKRPRLLIHYTSALQPGIP 79
           :| :|||| :|| | | : |::|: || : : |:|||| ||| ||||:  |:   |||
Db       1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy      80 SRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGGGTKLEIK 126
           |||||||| |::  || ||||| | ||| ||  :  |||||||:|||
Db      61 DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108


RESULT   9
Q99M37
ID   Q99M37      PRELIMINARY;      PRT;   238 AA.
AC   Q99M37;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   UNKNOWN (PROTEIN FOR MGC:5947).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY TUMOR;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002035; AAH02035.1; -.
SQ   SEQUENCE   238 AA;  26344 MW;  FB2B06A0B801330A CRC64;

  Query Match             46.7%;  Score 317.5;  DB 11;  Length 238;
  Best Local Similarity   47.0%;  Pred. No. 9.6e-27;
  Matches   62;  Conservative   26;  Mismatches   37;  Indels    7;  Gaps    3;

Qy       1 MRPSIQFLGLLLFWLHGAQCDIQMTQSPSSLSASLGGKVTITCKTSQDI-----NKYMAW 55
           |:  :: | :|:||:   :  |: |||:| ||  ||| : :|:|::|| |     | |: |
Db       1 MKLPVRLL-VLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEW 59

Qy      56 YQHKPGKRPRLLIHYTSALQPGIPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNL- 114
           |  |||: |:|||:  |    |:| |||||||| |::  || :| ||:  ||| |  ::
Db      60 YLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVP 119

Qy     115 WTFGGGTKLEIK 126
           :||| |||||||
Db     120 YTFGSGTKLEIK 131


RESULT  10
Q9UL85
ID   Q9UL85      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL85;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035029; AAD56265.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11761 MW;  FB1E43E7C7AFACCC CRC64;

  Query Match             45.6%;  Score 310;  DB 4;  Length 109;
  Best Local Similarity   56.0%;  Pred. No. 2.6e-26;
  Matches   61;  Conservative   18;  Mismatches   26;  Indels    4;  Gaps    2;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           :| |||||::|| | | : |::|  || |:  :|||| |||: |||||:  |    |||:
Db       1 EIVMTQSPATLSVSPGERATLSCWASQSISSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW---TFGGGTKLEIK 126
           |||||||| :::  ||:|: || | |:| || | |   |||||||:|||
Db      61 RFSGSGSGTEFTLTISSLQSEDFAIYHCQQY-NSWPPLTFGGGTKVEIK 108


RESULT  11
Q9UL86
ID   Q9UL86      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL86;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035028; AAD56264.1; -.
DR   HSSP; P01789; 1MCP.
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DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11928 MW;  243325F72C7DAC83 CRC64;


  Query Match             45.3%;  Score 308;  DB 4;  Length 109;
  Best Local Similarity   54.6%;  Pred. No. 4.3e-26;
  Matches   59;  Conservative   20;  Mismatches   27;  Indels    2;  Gaps    2;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDI-NKYMAWYQHKPGKRPRLLIHYTSALQPGIP 79
           :| :|||| :||   | : |::|: || : : |:|||| |||: |||||: ||:   |||
Db       1 EIVLTQSPGTLSLFPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIP 60

Qy      80 SRFSGSGSGRDYSFNISNLEPEDIATYYCLQY-DNLWTFGGGTKLEIK 126
           ||||||| |::  || ||||| | ||| ||  :::||| |||::||
Db      61 DRFSGSGSETDFTLTISRLEPEDFAVYYCQQYGSSIFTFGPGTKVDIK 108


RESULT  12
Q9UL83
ID   Q9UL83      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL83;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035031; AAD56267.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  9F9C5A92EBA96EEA CRC64;


  Query Match             44.9%;  Score 305.5;  DB 4;  Length 108;
  Best Local Similarity   53.7%;  Pred. No. 8e-26;
  Matches   58;  Conservative   21;  Mismatches   26;  Indels    3;  Gaps    2;

Qy      21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80
           :| |||||::|| | | : |::|: || ::  :|||| |||: |||||:  |    |||:
Db       1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYCASTRATGIPA 60

Qy      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLW--TFGGGTKLEIK 126
           |||||||| :::  ||:|: || | |||  |:| |  ||| |||::||
Db      61 RFSGSGSGTEFTLTISSLQPEDFAVYYCQHYNN-WPFTFGPGTKVDIK 107


RESULT  13
Q9U410
ID   Q9U410      PRELIMINARY;      PRT;   106 AA.
AC   Q9U410;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE   VARIABLE REGION (FRAGMENT).
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC   Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC   Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT   "Amplification, cloning and sequence analysis of the light chain
RT   variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT   Schistosoma japonicum.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF207620; AAF19434.1; -.
DR   HSSP; P01679; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     106    106
SQ   SEQUENCE   106 AA;  11478 MW;  F20F544426BAE63E CRC64;


  Query Match             44.0%;  Score 299;  DB 5;  Length 106;
  Best Local Similarity   57.7%;  Pred. No. 4e-25;
  Matches   60;  Conservative   14;  Mismatches   28;  Indels    2;  Gaps    2;

Qy      24 MTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPSRFS 83
           :|||: :||| | |||:||  |  :: |: ||  |||  |||||: || |  |:| |||
Db       4 LTQSPAIMSASPGEKVTMTCSASSSVS-YVYWYLQKPGSSPRLLIYDTSNLASGVPVRFS 62

Qy      84 GSGSGRDYSFNISNLEPEDIATYYCLQYDNL-WTFGGGTKLEIK 126
           |||||  ||  || :| || ||||| |: :  :||| |||||:|
Db      63 GSGSGTSYSLTISRMEAEDAATYYCQQWTSYPFTFGSGTKLELK 106


RESULT  14
Q9ERZ9
ID   Q9ERZ9      PRELIMINARY;      PRT;   107 AA.
AC   Q9ERZ9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT   "Cloning and sequencing of the light chain fragment of variable region
RT   genes of an anti-hTNF-a monoclonal antibody.";
RL   J. Cell. Mol. Immunol. 12:21-26(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT   "Construction and sequencing of the single-chain antibody gene of a
RT   human TNF-alpha specific monoclonal antibody.";
RL   Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF262753; AAG23804.1; -.
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DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11784 MW;  2B15EEA6604A26C3 CRC64;


  Query Match             43.5%;  Score 295.5;  DB 11;  Length 107;
  Best Local Similarity   51.4%;  Pred. No. 9.7e-25;
  Matches   55;  Conservative   21;  Mismatches   24;  Indels    7;  Gaps    2;

Qy      24 MTQSPSSLSASLGGKVTITCKTSQDI------NKYMAWYQHKPGKRPRLLIHYTSALQPG 77
           ||||||||: |:| |||::||:|| :        |:|||| |||: | ||::: |  : |
Db       1 MTQSPSSLAMSVGQKVTMSCKSSQSVLNSNTQKNYLAWYQKKPGQSPELLVYFASTRESG 60

Qy      78 IPSRFSGSGSGRDYSFNISNLEPEDIATYYCLQ-YDNLWTFGGGTKL 123
           :| || ||||| |::  ||::: ||:| |:| | |   :||| ||||
Db      61 VPDRFMGSGSGTDFTLTISSVQTEDLADYFCQQHYRTPFTFGSGTKL 107


RESULT  15
Q9JL78
ID   Q9JL78      PRELIMINARY;      PRT;   101 AA.
AC   Q9JL78;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A.CA;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206028; AAF69326.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     101    101
SQ   SEQUENCE   101 AA;  10778 MW;  0A7F65E6A7E6F14D CRC64;


  Query Match             43.0%;  Score 292.5;  DB 11;  Length 101;
  Best Local Similarity   56.4%;  Pred. No. 1.9e-24;
  Matches   57;  Conservative   16;  Mismatches   25;  Indels    3;  Gaps    2;

Qy      29 SSLSASLGGKVTITCKTSQDI-NKYMAWYQHKPGKRPRLLIHYTSALQPGIPSRFSGSGS 87
           ::::|| | |:|||| | | : |: ||| |||  |:|||: || |  |:|:|||||||
Db       1 TTMAASPGEKITITCSASSSISSNYLHWYQQKPGFSPKLLIYRTSNLASGVPTRFSGSGS 60

Qy      88 GRDYSFNISNLEPEDIATYYCLQYDNL--WTFGGGTKLEIK 126
           |  ||  |  :| ||:||||| |  ::  :||||||||||
Db      61 GTSYSLTIGTMEAEDVATYYCQQGSSIPRYTFGGGTKLEIK 101


Search completed: May  7, 2002, 12:31:42
Job time: 638 sec
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 12:22:24 ; Search time 67.39 Seconds
(without alignments)
153.884 Million cell updates/sec

Title: US-09-155-739-4
Perfect score: 746
Sequence: 1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_1101:*
1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
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20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	746	100.0	140	16	AAR81327	Mouse VLA-4 antibo
2	746	100.0	140	18	AAW22410	Alpha-4 integrin m
3	645	86.5	123	16	AAR81330	Mouse anti-VLA-4 a
4	633	84.9	136	17	AAW04379	Chimaeric human/mu
5	629	84.3	140	12	AAR11384	Variable gamma hea
6	625	83.8	136	16	AAR76664	Murine ONS-21 anti
7	595	79.8	136	14	AAR41679	V heavy chain of r
8	593.5	79.6	137	18	AAW21845	Heavy chain variab
9	591	79.2	138	19	AAW63828	Human Mab #117-10C
10	584	78.3	142	16	AAR81333	Human VLA-4 reshap
11	584	78.3	142	18	AAW22428	Humanised alpha-4
12	576.5	77.3	135	21	AAB07967	Amino acid sequenc
13	570.5	76.5	137	17	AAR95948	HNK-20 variable he
14	544	72.9	123	16	AAR81323	Humanized VLA-4 an
15	539.5	72.3	135	21	AAB07969	A heavy chain vari
16	537	72.0	123	18	AAW22413	Humanised alpha-4
17	535.5	71.8	437	19	AAW37738	Nucleotide sequenc
18	524.5	70.3	122	21	AAY53590	Heavy chain from a
19	521.5	69.9	120	14	AAR30767	Heavy chain variab
20	521.5	69.9	120	19	AAW44121	Heavy chain variab
21	518.5	69.5	113	15	AAR60527	Heavy chain variab
22	517	69.3	143	15	AAR59942	Anti-VLA4 rAb huma
23	516.5	69.2	120	16	AAR79889	Anti-EGFR antibody
24	516	69.2	121	20	AAW96741	Heavy chain variab
25	513	68.8	121	20	AAW96744	Heavy chain variab
26	511	68.5	120	14	AAR39817	HP1/2 Vh. Homo sa
27	511	68.5	120	15	AAR58749	Anti-VLA4 Ab HP1/2
28	511	68.5	120	20	AAY23984	Antibody HP1/2 hea
29	511	68.5	120	20	AAY01033	Anti VLA-4 antibod
30	511	68.5	120	22	AAB73462	Murine anti-VLA-4
31	509.5	68.3	126	12	AAR15439	Heavy chain variab
32	508	68.1	120	14	AAR39566	Sequence of the va
33	505.5	67.8	138	21	AAY56873	MAb CT-M-01 heavy
34	505.5	67.8	139	18	AAW29750	Anti-HMFG MAb CTMO
35	504	67.6	254	20	AAY30117	Murine anti-botuli
36	504	67.6	254	20	AAY30119	Murine anti-botuli
37	504	67.6	254	20	AAY30121	Murine anti-botuli
38	504	67.6	254	20	AAY30123	Murine anti-botuli
39	503	67.4	136	22	AAB82701	VEGF antagonist an
40	502	67.3	136	16	AAR76681	Human/murine chime
41	502	67.3	136	17	AAW04396	Chimaeric human/mu
42	501.5	67.2	116	12	AAR15437	Heavy chain variab
43	501.5	67.2	240	12	AAR15443	Single chain Fv fr
44	501	67.2	119	19	AAW63820	Human Mab #117-10C
45	501	67.2	248	19	AAW63830	Transformant CDM/1

ALIGNMENTS

RESULT 1
AAR81327
ID AAR81327 standard; Protein; 140 AA.
XX
AC AAR81327;
XX
DT 23-MAR-1996 (first entry)
XX
DE Mouse VLA-4 antibody 21.6 light heavy variable region.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.
XX
OS Mus musculus.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1..19
FT		/note= "signal peptide"
FT	Region	20..49
FT		/note= "framework region 1"
FT	Region	50..54
FT		/note= "complementarity determining region 1"
FT	Region	55..68
FT		/note= "framework region 2"
FT	Region	69..85
FT		/note= "complementarity determining region 2"
FT	Region	86..117
FT		/note= "framework region 3"
FT	Region	118..131
FT		/note= "complementarity determining region 3"
FT	Region	132..140
FT		/note= "framework region 4"

XX
PN WO9519790-A1.

XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
DR N-PSDB; AAQ99892.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating
PT inflammatory disease.
XX
PS Disclosure; Fig 2; 105pp; English.
XX
CC The sequence represents the mouse antibody 21.6 heavy chain variable
CC region directed against leukocyte adhesion molecule VLA-4. Cloned
CC cDNA sequences of mouse 21.6 VH and VL (see AAQ99889) regions are
CC linked to human constant regions in the construction of a humanized
CC antibody against VLA-4. The 5' and 3' ends of the mouse cDNAs are
CC modified using PCR primers (See AAQ99895-98) and then subcloned into
CC mammalian cell expression vectors containing human kappa or gamma-1
CC constant regions. In the humanized heavy chain, amino acids H27,
CC H28, H29, H30, H44 nd H71 in the human HC VR framework are replaced
CC by the amino acid present in the equivalent position of the mouse
CC 21.6 Ig H chain. Plasmids encoding the chimeric antibodies are
CC transfected into COS cells. The humanized antibodies can be used
CC to inhibit adhesion of a leukocyte to an endothelial cell and
CC to treat inflammatory diseases such as multiple sclerosis. They
CC can also be used in the treatment of stroke, cerebral traumas,
CC meningitis or encephalitis. The antibodies can also be used for
CC detecting VLA-4, for affinity purification or for generating
CC anti-idiotype antibodies.
XX
SQ Sequence 140 AA;

Query Match 100.0%; Score 746; DB 16; Length 140;
Best Local Similarity 100.0%; Pred. No. 5.9e-60;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mkcswvmfflmavvtgvnsevqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrp 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 eqglewigridpangytkydpkfqgkatitadtssntaylqlssltsedtavyfcaregy 120

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           ||||||||||||||||||||
Db     121 ygnygvyamdywgqgtsvtv 140
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RESULT 2
AAW22410
ID AAW22410 standard; Protein; 140 AA.
XX
AC AAW22410;
XX
DT 08-DEC-1997 (first entry)
XX
DE Alpha-4 integrin mouse MAb 21.6 VH region.
XX
KW Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW transplant rejection; graft versus host disease; nephritis;
KW atopic dermatitis; psoriasis; myocardial ischaemia;
KW acute leukocyte mediated lung injury; therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Leader
FT Region 20..49
FT /label= FR1
FT /note= "framework region 1"
FT Region 50..54
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 55..68
FT /label= FR2
FT /note= "framework region 2"
FT Region 69..85
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 86..117
FT /label= FR3
FT /note= "framework region 3"
FT Region 118..131
FT /label= CDR3
FT /note= "complementarity determining region 3"
FT Region 132..140
FT /label= FR4
FT /note= "framework region 4"
XX
PN WO9718838-A1.
XX
PD 29-MAY-1997.
XX
PF 21-NOV-1996; 96WO-US18807.
XX
PR 21-NOV-1995; 95US-0561521.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR WPI; 1997-297879/27.
DR N-PSDB; AAT74760.
XX
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS Claim 18; Page 69-70; 107pp; English.
XX
CC This polypeptide comprises the heavy chain variable region (VH) of
CC mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
CC complementarity determining regions (CDRs) of the 21.6 VH can be
CC incorporated into a human 21/28'CL framework to produce a claimed
CC humanised 21.6 VH (see AAW22413) and a claimed humanised 21.6
CC antibody that is used in the manufacture of a medicament for
CC treating a disease selected from asthma, atherosclerosis, AIDS,
CC dementia, diabetes, inflammatory bowel disease, rheumatoid
CC arthritis, transplant rejection, graft versus host disease, tumour
CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC ischaemia, and acute leukocyte mediated lung injury. The antibody
CC may also be used in the affinity purification of alpha-4 integrin
CC for use as a vaccine or an immunogen. It is also useful for
CC generating idiotypic antibodies. The humanised antibodies of the
CC invention have a half-life in the human circulation essentially
CC equivalent to that of naturally occurring human antibodies.
XX
SQ Sequence 140 AA;

Query Match 100.0%; Score 746; DB 18; Length 140;
Best Local Similarity 100.0%; Pred. No. 5.9e-60;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 mkcswvmfflmavvtgvnsevqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrp 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 eqglewigridpangytkydpkfqgkatitadtssntaylqlssltsedtavyfcaregy 120

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           ||||||||||||||||||||
Db     121 ygnygvyamdywgqgtsvtv 140


RESULT   3
AAR81330
ID   AAR81330 standard; Protein; 123 AA.
XX
AC   AAR81330;
XX
DT   02-APR-1996  (first entry)
XX
DE   Mouse anti-VLA-4 antibody 21.6 heavy chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Region          1..30
FT                   /label= FR1
FT                   /note= "mouse heavy chain variable framework
FT                        region 1"
FT   Region          31..35
FT                   /label= CDR1
FT                   /note= "mouse heavy chain variable complementarity
FT                        determining region 1"
FT   Region          36..49
FT                   /label= FR2
FT                   /note= "mouse heavy chain variable framework
FT                        region 2"
FT   Region          50..66
FT                   /label= CDR2
FT                   /note= "mouse heavy chain variable complementarity
FT                        determining region 2"
FT   Region          67..98
FT                   /label= FR3
FT                   /note= "mouse heavy chain variable framework
FT                        region 3"
FT   Region          99..112
FT                   /label= CDR3
FT                   /note= "mouse heavy chain variable complementarity
FT                        determining region 3"
FT   Region          113..123
FT                   /label= FR4
FT                   /note= "mouse heavy light chain variable framework
FT                        region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Page 68; 105pp; English.
XX
CC   The sequence represents the mouse anti-VLA-4 antibody 21.6 heavy chain
CC   variable region (without signal sequence). Cloned cDNA CDR sequences of
CC   mouse 21.6 variable light and variable heavy regions are linked to human
CC   constant framework regions of the REI antibody for the light chain and
CC   the 2*CL antibody for the heavy chain in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45, L49,
CC   L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC   acid present in the equivalent position of the mouse 21.6 Ig light
CC   chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC   cells. The humanized antibodies can be used to inhibit adhesion of a
CC   leukocyte to an endothelial cell and to treat inflammatory diseases such
CC   as multiple sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC   used for detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   123 AA;


  Query Match             86.5%;  Score 645;  DB 16;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-51;
  Matches  121;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 evqlqqsgaelvkpgasvklsctasgfnikdtyihcvkqrpegglewigridpangytky 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 dpkfqgkatitadtssntaylqlssltsedtavyfcaregyygnygvyamdywgqgtsvt 120

Qy     140 V 140
           |
Db     121 v 121


RESULT   4
AAW04379
ID   AAW04379 standard; Protein; 136 AA.
XX
AC   AAW04379;
XX
DT   04-DEC-1996  (first entry)
XX
DE   Chimaeric human/murine MAb ONS-M21 variable heavy region.
XX
KW   Heavy; variable region; murine; human; myeloblastoma; chimaera;
KW   monoclonal antibody; chimera; single stranded Fv region;
KW   low human antigenicity; diagnosis; treatment; cerebral tumour;
KW   reshaped.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= sig_peptide
FT   Peptide         20..136
FT                   /label= mat_peptide
FT   Region          50..54
FT                   /label= CDR_1
FT   Region          69..85
FT                   /label= CDR_2
FT   Region          118..125
FT                   /label= CDR_3
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XX
PN   JP08169900-A.
XX
PD   02-JUL-1996.
XX
PF   18-NOV-1994;   94JP-0285057.
XX
PR   18-OCT-1994;   94JP-0252166.
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS ) CHUGAI PHARM CO LTD.
XX
DR   WPI; 1996-358509/36.
DR   N-PSDB; AAT38600.
XX
PT   Reshaped anti-human myeloblastoma cell human antibody - has low
PT   human antigenicity, and is therefore useful for diagnosis and
PT   treatment of cerebral tumours, e.g. myeloblastoma
XX
PS   Example 2; Page 22; 45pp; Japanese.
XX
CC   The present sequence is the variable heavy region of the
CC   chimaeric human/murine monoclonal antibody (MAb) ONS-M21. The MAb
CC   was prepd. by combining light and heavy variable region DNA,
CC   from a murine anti-human myeloblastoma cell MAb, with human light
CC   and heavy constant region sequences, respectively to produce
CC   chimaeric human/murine light and heavy chain DNA mols.. A
CC   recombinant vector for the expression of the heavy and light chain
CC   DNA mols. was prepd., and used to transform a host cell. The host
CC   cell was then cultured, and the expression prods. of the heavy and
CC   light chain DNA mols. sepd. and connected with a peptide linker to
CC   produce a single stranded Fv region. The reshaped Fv region has
CC   low human antigenicity, and is therefore expected to be useful as
CC   an agent for the diagnosis and treatment of cerebral tumours,
CC   e.g. myeloblastoma.
XX
SQ   Sequence   136 AA;
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  Query Match             84.9%;  Score 633;  DB 17;  Length 136;
  Best Local Similarity   89.3%;  Pred. No. 8.8e-50;
  Matches  125;  Conservative    2;  Mismatches    7;  Indels    6;  Gaps    2;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db       1 mkcswvmfflmavvtgvnsevqlqqsgaelvkpgasvklsctasgfnikdtyihwakqrp 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||||||||:| |||||||||||||||||||||||||||||||||||||:||   |
Db      61 eqglewigridpadgntkydpkfqgkatitadtssntaylqlssltsedtavyyca-say 119

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           | |      ||||||||||
Db     120 yvn-----qdywgqgtsvtv 134
```

```
RESULT   5
AAR11384
ID   AAR11384 standard; Protein; 140 AA.
XX
AC   AAR11384;
XX
DT   08-MAY-1991  (first entry)
XX
DE   Variable gamma heavy chain of T84.66 monoclonal antibody.
XX
KW   MAb T84.66; gamma heavy chain; carcinoembryonic antigen; CEA;
KW   human adenocarcinoma; mouse-human chimaeric antibody.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         20..38
FT                   /label= tryptic peptide
FT                   /note= "sequenced as peptide fragment"
FT   Peptide         39..49
FT                   /label= tryptic peptide
FT                   /note= "sequenced as peptide fragment"
FT   Peptide         55..59
FT                   /label= tryptic peptide
FT                   /note= "sequenced as peptide fragment"
FT   Region          50..54
FT                   /label= complementarity determining region
FT   Region          69..85
FT                   /label= complementarity determining region
FT   Region          118..130
FT                   /label= complementarity determining region
XX
PN   WO9101990-A.
XX
PD   21-FEB-1991.
XX
PF   19-JUL-1990;   90WO-US04049.
XX
PR   26-JUL-1989;   89US-0385102.
XX
PA   (CITY ) CITY OF HOPE.
XX
PI   Shively JE,  Riggs AD,  Neumaier M;
XX
DR   WPI; 1991-073486/10.
DR   N-PSDB; AAQ11098.
XX
PT   Novel anti-CEA antibody - comparable to ATCC Accession No. BH
PT   8747, produced by recombinant DNA, used in diagnosis of tumours
XX
PS   Claim 4; Page 18; 24pp; English.
XX
CC   The heavy chain variable region of murine MAb 84.66 was cloned and
CC   sequenced. It was used to produce mouse V-human C antibodies with high
CC   affinity for CEA. Chimaeric murine-human anti-CEA Abs are used to
CC   diagnose human colon adenocarcinomas.
CC   See also AAQ10834-Q10848.
XX
SQ   Sequence   140 AA;
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  Query Match             84.3%;  Score 629;  DB 12;  Length 140;
  Best Local Similarity   87.9%;  Pred. No. 2.1e-49;
  Matches  123;  Conservative    6;  Mismatches    9;  Indels    2;  Gaps    1;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||:|||||||||||||||||||||:|||||||||||||||||||:| |||||
Db       1 mkcswvifflmavvtgvnsevqlqqsgaelvepgasvklsctasgfnikdtymhwvkqrp 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||||||||| :|| |||||||||||||||||||:|||||||||:||  ||
Db      61 eqglewigridpangnskyvpkfqgkatitadtssntaylqltsltsedtavyycapfgy 120

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           |     ||| ||||||||||
Db     121 y--vsdyamaywgqgtsvtv 138
```

```
RESULT   6
AAR76664
ID   AAR76664 standard; Protein; 136 AA.
XX
AC   AAR76664;
XX
DT   16-JAN-1996  (first entry)
XX
DE   Murine ONS-21 antibody variable heavy chain.
XX
KW   Plasmid pUC-M21-V(H); murine; ONS-M21 antibody; chimeric protein;
KW   medulloblastoma; brain tumour; treatment; diagnosis.
```

```
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= sig_peptide
FT   Peptide         20..136
FT                   /label= mat_peptide
XX
PN   WO9514041-A1.
XX
PD   26-MAY-1995.
XX
PF   19-OCT-1994;   94WO-JP01763.
XX
PR   19-NOV-1993;   93JP-0291078.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Ohtomo T,  Sato K,  Tsuchiya M;
XX
DR   WPI; 1995-200347/26.
DR   N-PSDB; AAQ94485.
XX
PT   Reconstituted antibody against human medullo:blastoma cells -
PT   contains high proportion of human antibody origin and has low
PT   antigenicity
XX
PS   Claim 14; Page 59; 120pp; Japanese.
XX
CC   AAQ94485 is the plasmid pUC-M21-V(H), which encodes AAR76664 the
CC   murine antibody ONS-21 variable heavy chain. The plasmid was
CC   used in the construction of an expression vector, contg. cDNA
CC   encoding a human/murine chimeric antibody, reactive with
CC   human medulloblastoma (a brain tumour) cells. The chimeric
CC   antibody can be used in the diagnosis and treatment of this
CC   disease.
XX
SQ   Sequence   136 AA;
```

```
  Query Match             83.8%;  Score 625;  DB 16;  Length 136;
  Best Local Similarity   88.6%;  Pred. No. 4.6e-49;
  Matches  124;  Conservative    2;  Mismatches    8;  Indels    6;  Gaps    2;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |||||||||||||||||||||||| |||||||||||||||||||||||||  ||||
Db       1 mkcswvmfflmavvtgvnsevqlqqsraelvkpgasvklsctasgfnikdtyihwakqrp 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||||||||:| |||||||||||||||||||||||||||||||||||:||   |
Db      61 eqglewigridpadgntkydpkfqgkatitadtssntaylqlssltsedtavyyca-say 119

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           | |      ||||||||||
Db     120 yvn-----qdywgqgtsvtv 134
```

```
RESULT   7
AAR41679
ID   AAR41679 standard; Protein; 136 AA.
XX
AC   AAR41679;
XX
DT   24-MAR-1994  (first entry)
XX
DE   V heavy chain of recombinant anti-feline calcivirus antibody.
XX
KW   Antibody; feline calcivirus; FCV; neutralise; heavy chain; virus;
KW   infection; diagnosis; treatment; prophylaxis.
XX
OS   Synthetic.
XX
```

```
FH   Key             Location/Qualifiers
FT   Domain          47..54
FT                   /label= Complementary Determining Region 1.
FT   Domain          69..86
FT                   /label= Complementary Determining Region 2.
FT   Domain          118..125
FT                   /label= Complementary Determining Region 3.
XX
PN   EP561194-A.
XX
PD   22-SEP-1993.
XX
PF   26-FEB-1993;   93EP-0103066.
XX
PR   28-FEB-1992;   92JP-0079189.
XX
PA   (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
XX
PI   Kimachi K,  Maeda H,  Mikami T,  Nishiyama K,  Tohya Y;
PI   Tokiyoshi S;
XX
DR   WPI; 1993-296521/38.
DR   N-PSDB; AAQ48001.
XX
PT   Anti-feline calcivirus recombinant antibody - used to treat,
PT   prevent and diagnosis infection and is safe but effective in cats
XX
PS   Claim 1-2; Figure 3; 36pp; English.
XX
CC   The gene fragment encoding the V heavy chain region is used to
CC   produce a genetically engineered antibody capable of reacting
CC   specifically with feline calcivirus (FCV).  The antibody can be used
CC   to treat, prevent and diagnose FCV infection.  It has a broad virus-
CC   neutralising spectrum and can be used to neutralise viruses which
CC   have acquired immunity to other neutralising antibodies.
XX
SQ   Sequence   136 AA;
```

```
  Query Match             79.8%;  Score 595;  DB 14;  Length 136;
  Best Local Similarity   82.9%;  Pred. No. 2.3e-46;
  Matches  116;  Conservative    8;  Mismatches   10;  Indels    6;  Gaps    1;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||:|||||||||||||||||||||||||||||:|||||||||||||:| |||||
Db       1 mkcswvifflmavvtgvnsevqlqqsgaelvkpgasvrlsctasgfnikdtymhwvkqrp 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||||||||| |||||:|||||||||||| ||||||::|||||||||:||   |
Db      61 eqglewigridpangntkydprfqgkatitadtsfntaylqvnsltsedtavyycasggn 120

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
                 : |||||| |||
Db     121 aw------laywgqgtlvtv 134
```

```
RESULT   8
AAW21845
ID   AAW21845 standard; Protein; 137 AA.
XX
AC   AAW21845;
XX
DT   19-DEC-1997  (first entry)
XX
DE   Heavy chain variable region of KM1486 antibody.
XX
KW   Complementarity determining region; CDR; heavy chain; treatment;
KW   variable region; murine; mouse; human; interleukin 5; IL-5;
KW   receptor; alpha chain; monoclonal antibody; hybridoma; detection;
KW   assay; diagnosis; allergic respiratory disease;
KW   chronic bronchitis.
XX
OS   Mus spp.
```

```
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= sig_peptide
FT   Peptide         20..137
FT                   /label= mat_peptide
FT   Region          50..54
FT                   /label= complementarity_determining_region_1
FT   Region          69..85
FT                   /label= complementarity_determining_region_2
FT   Region          118..126
FT                   /label= complementarity_determining_region_3
XX
PN   WO9710354-A1.
XX
PD   20-MAR-1997.
XX
PF   11-SEP-1996;   96WO-JP02588.
XX
PR   11-SEP-1995;   95JP-0232384.
XX
PA   (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI   Anazawa H,  Furuya A,  Hanai N,  Iida A,  Koike M;
PI   Nakamura K,  Takatsu K;
XX
DR   WPI; 1997-202249/18.
DR   N-PSDB; AAT73612.
XX
PT   Antibody against alpha-chain of human interleukin 5 receptor -
PT   useful for diagnosis and treatment of respiratory allergic diseases,
PT   e.g. chronic bronchitis
XX
PS   Example 2; Pages 124-125; 238pp; Japanese.
XX
CC   The present sequence is the heavy chain variable region of the
CC   murine anti-human interleukin 5 receptor alpha chain (hIL-5R alpha)
CC   monoclonal antibody (MAb) KM1486. KM1486 is produced by the hybridoma
CC   FERM BP-5651, which was prepared by immunising Balb/c mice with
CC   hIL-5R alpha, fusing spleen cells obtained from the mice with mouse
CC   myeloma P3-U1 cells and screening the resultant hybridomas. The MAb
CC   can be used to detect or assay for hIL-5R alpha and cells
CC   expressing it on their surface, especially to diagnose allergic
CC   respiratory diseases, e.g. chronic bronchitis. It can also be used
CC   to treat such diseases.
XX
SQ   Sequence   137 AA;
```

```
  Query Match             79.6%;  Score 593.5;  DB 18;  Length 137;
  Best Local Similarity   82.9%;  Pred. No. 3.2e-46;
  Matches  116;  Conservative    6;  Mismatches   13;  Indels    5;  Gaps    1;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||:|||||||||||||||||||||||||||| |||||||||||||:| |||||
Db       1 mkcswvifflmavvtgvnsevqlqqsgaelvkpgasvnlsctasgfnikdtymhwvkqrp 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||||||||| || ||||| |||| ||||||||||||||||||||:|
Db      61 eqglewigridpangntksdpkfqakatiaadtssntaylqlssltsedtavyyct---- 116

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
             |   :   |||||||::||
Db     117 -gglrlrffdywgqgttltv 135


RESULT   9
AAW63828
ID   AAW63828 standard; Protein; 138 AA.
XX
AC   AAW63828;
XX
DT   28-SEP-1998  (first entry)
```

```
XX
DE   Human Mab #117-10C heavy chain variable region protein fragment.
XX
KW   Interleukin-18: IL-18; human; treatment; autoimmune disease; Mab;
KW   immunosuppressant; inhibitor; receptor protein; detection; heavy chain;
KW   monoclonal antibody; Mab; variable region.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..19
FT                   /label= signal
FT   Protein         20..138
FT                   /label= Mab 117-10C heavy chain variable region
XX
PN   EP850952-A1.
XX
PD   01-JUL-1998.
XX
PF   23-DEC-1997;   97EP-0310555.
XX
PR   28-JUL-1997;   97JP-0215490.
PR   26-DEC-1996;   96JP-0356426.
PR   21-FEB-1997;   97JP-0052526.
PR   06-JUN-1997;   97JP-0163490.
XX
PA   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
PI   Kunikata T,  Kurimoto M,  Torigoe K,  Ushio S;
XX
DR   WPI; 1998-335317/30.
DR   N-PSDB; AAV44000.
XX
PT   New interleukin-18 receptor protein used to inhibit interleukin-18,
PT   to treat autoimmune disease and as immunosuppressant - and new
PT   monoclonal antibody and hybridoma used to detect interleukin -18
PT   receptor protein
XX
PS   Example 3.3a; Page 22; 35pp; English.
XX
CC   This sequence represents the human monoclonal antibody (Mab) #117-10C
CC   heavy chain variable region which is used in a method involved in
CC   neutralising IL-18 or to treat autoimmune diseases or as an
CC   immunosuppressant using anti-IL-18 antibodies which can inhibit IL-18.
CC   Such antibodies can also be used to detect the IL-18 receptor protein
CC   (labelled with an enzyme or a radioactive or fluorescent substance). The
CC   protein is used to treat e.g. graft rejection, pernicious anaemia,
CC   atrophic gastritis, insulin-resistant diabetes, Wegener granulomatosis,
CC   discoid lupus erythematosis, ulcerative colitis, cold-agglutinin-relating
CC   diseases, Goodpasture's syndrome, primary biliary cirrhosis, sympathetic
CC   ophthalmitis, hyperthyroidism, juvenile onset type diabetes, Sjogren
CC   syndrome, autoimmune hepatitis, autoimmune haemolytic anaemia, myasthenia
CC   gravis, systemic scleroderma, systemic lupus erythematosus, polyleptic
CC   cold haemoglobinuria, polymyositis, periarteritis nodosa, multiple
CC   sclerosis, Addison's disease, purpura haemorrhagica, Basedow's disease,
CC   leukopaenia, Behcet's disease, climacterium praecox, rheumatoid
CC   arthritis, rheumatopyra, chronic thyroiditis, Hodgkin's disease, HIV,
CC   asthma, atopic dermatitis, allergic nastitis, pollinosis,
CC   apitoxin-allergy and septic shock resulting from production or
CC   administration of excessive gamma interferon (IFN-gamma).
XX
SQ   Sequence   138 AA;
```

```
  Query Match             79.2%;  Score 591;  DB 19;  Length 138;
  Best Local Similarity   83.0%;  Pred. No. 5.5e-46;
  Matches  117;  Conservative    4;  Mismatches   14;  Indels    6;  Gaps    2;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||  ||||||||||||||||||||||||||||||||| ||||||| ||: |||||
Db       1 mkcswvflflmavvtgvnsevqlqqsgaelvkpgasvklscttsgfnikdiyiywvkqrp 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
```

```
          |||||||:|||||||| ||| | || |||||||||||||||| |||||||||||:||| |
Db     61 egglewvgridpangdtkygpnfqdkatitadtssntaylqlrsltsedtavyycarrgn 120

Qy    121 YG-NYGVYAMDYWGQGTSVTV 140
          ||  :|     |||||| |||
Db    121 ygagfg-----ywgqgtlvtv 136
```

RESULT 10
AAR81333
ID AAR81333 standard; Protein; 142 AA.
XX
AC AAR81333;
XX
DT 23-MAR-1996 (first entry)
XX
DE Human VLA-4 reshaped antibody 21.6 light heavy variable region.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1..19
FT		/note= "signal peptide"
FT	Region	20..49
FT		/note= "framework region 1"
FT	Region	50..54
FT		/note= "complementarity determining region 1"
FT	Region	55..68
FT		/note= "framework region 2"
FT	Region	69..85
FT		/note= "complementarity determining region 2"
FT	Region	86..117
FT		/note= "framework region 3"
FT	Region	118..131
FT		/note= "complementarity determining region 3"
FT	Region	132..142
FT		/note= "framework region 4"

XX
PN WO9519790-A1.
XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
DR N-PSDB; AAQ99894.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating
PT inflammatory disease.
XX
PS Disclosure; Fig 11; 105pp; English.
XX
CC The sequence represents the human reshaped antibody 21.6 heavy
CC chain variable region against leukocyte adhesion molecule VLA-4.
CC Cloned cDNA sequences of mouse 21.6 VH (AAQ99892) and VL (AAQ99889)
CC regions are linked to human constant regions in the construction
CC of a humanized antibody against VLA-4. The 5' and 3' ends of the
CC mouse cDNAs are modified using PCR primers (AAQ99895-98) and then
CC subcloned into mammalian cell expression vectors containing human
CC kappa or gamma-1 constant regions. In the humanized heavy chain,
CC amino acids H27, H28, H29, H30, H44 nd H71 in the human HC VR
CC framework are replaced by the amino acid present in the equivalent
CC position of the mouse 21.6 Ig H chain. Plasmids encoding the
CC chimeric antibodies are transfected into COS cells. The humanized
CC antibodies can be used to inhibit adhesion of a leukocyte to an
CC endothelial cell and to treat inflammatory diseases such as multiple
CC sclerosis. They can also be used in the treatment of stroke,
CC cerebral traumas, meningitis or encephalitis. The antibodies can
CC also be used for detecting VLA-4, for affinity purification or for
CC generating anti-idiotype antibodies.
XX
SQ Sequence 142 AA;

```
  Query Match             78.3%;  Score 584;  DB 16;  Length 142;
  Best Local Similarity   77.1%;  Pred. No. 2.4e-45;
  Matches  108;  Conservative   15;  Mismatches   17;  Indels    0;  Gaps    0;

Qy      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          |  :| :| |:||  | :|:||| ||||: |||||||:|| |||||||||||| |:| |
Db      1 mdwtwrvfcllavapgahsqvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqap 60

Qy     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          | |||:||||||||||||||||: |||||||::|||::|||| |||||||:||||||
Db     61 gqrlewmgridpangytkydpkfqgrvtitadtsastaymelsslrsedtavyycaregy 120

Qy    121 YGNYGVYAMDYWGQGTSVTV 140
          ||||||||||||||| |||
Db    121 ygnygvyamdywgqgtlvtv 140
```

RESULT 11
AAW22428
ID AAW22428 standard; Protein; 142 AA.
XX
AC AAW22428;
XX
DT 09-DEC-1997 (first entry)
XX
DE Humanised alpha-4 integrin antibody 21.6 VL version Ha.
XX
KW Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW transplant rejection; graft versus host disease; nephritis;
KW atopic dermatitis; psoriasis; myocardial ischaemia;
KW acute leukocyte mediated lung injury; therapy.
XX
OS Chimeric Mus musculus;
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1..19
FT		/label= Leader
FT	Protein	20..142
FT		/label= Mat_protein
FT		/note= "VH version Ha (Claim 25)"
FT	Region	20..49
FT		/label= FR1
FT		/note= "21/28'CL framework region 1"
FT	Region	50..55
FT		/label= CDR1
FT		/note= "21.6 complementarity determining region 1"
FT	Region	55..67
FT		/label= FR2
FT		/note= "21/28'CL framework region 2"
FT	Region	68..85
FT		/label= CDR2
FT		/note= "21.6 complementarity determining region 2"
FT	Region	86..117
FT		/label= FR3
FT		/note= "21/28'CL framework region 3"
FT	Region	118..131
FT		/label= CDR3
FT		/note= "21.6 complementarity determining region 3"

FT Region 132..142
FT /label= FR4
FT /note= "21/28'CL framework region 4"
XX
PN WO9718838-A1.
XX
PD 29-MAY-1997.
XX
PF 21-NOV-1996; 96WO-US18807.
XX
PR 21-NOV-1995; 95US-0561521.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR WPI; 1997-297879/27.
DR N-PSDB; AAT74789.
XX
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS Example 6; Fig 11; 107pp; English.
XX
CC This polypeptide, designated Ha, comprises the heavy chain variable
CC region (VH) of a humanised alpha-4 integrin antibody 21.6 (see also
CC AAW22413). It is composed of complementarity determining regions from
CC the VH region (see AAW22410) of mouse alpha-4 integrin monoclonal
CC antibody 21.6 and a modified human 21/28'CL framework. It can be
CC expressed in mammalian host cells following PCR amplification and
CC mutagenesis of appropriate mouse and human DNA sequences. The
CC humanised 21.6 VH and a humanised 21.6 VL (see AAW22412) can be used
CC to produce a claimed humanised 21.6 antibody that is useful in the
CC manufacture of a medicament for treating asthma, atherosclerosis,
CC AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC arthritis, transplant rejection, graft versus host disease, tumour
CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC ischaemia, and acute leukocyte mediated lung injury. The humanised
CC antibody has a half-life in the human circulation essentially
CC equivalent to that of naturally occurring human antibodies.
XX
SQ Sequence 142 AA;

Query Match 78.3%; Score 584; DB 18; Length 142;
Best Local Similarity 77.1%; Pred. No. 2.4e-45;
Matches 108; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
Db 1 mdwtwrvfcllavapgahsqvqlvqsgaevkkpgasvkvsckasgfnikdtyihwvrqap 60

Qy 61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
Db 61 gqrlewmgridpangytkydpkfqgrvtitadtsastaymelsslrsedtavyycaregy 120

Qy 121 YGNYGVYAMDYWGQGTSVTV 140
Db 121 ygnygvyamdywgqgtlvtv 140

RESULT 12
AAB07967
ID AAB07967 standard; Protein; 135 AA.
XX
AC AAB07967;
XX
DT 14-NOV-2000 (first entry)
XX
DE Amino acid sequence of heavy chain variable region of 1F1 antibody.
XX
KW Antibody 1F1; B7 molecule; B7; humanised immunoglobulin;
KW autoimmune disease; infectious disease; inflammatory disorder;
KW systemic lupus erythematosus; diabetes mellitus; insulitis; asthma;
KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW multiple sclerosis; transplant rejection; proliferative disease;
KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW aplastic anaemia; myeloid dysplasia syndrome.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "signal peptide"
FT Protein 20..135
FT /note= "mature protein"
FT Region 50..54
FT /note= "complementarity determining region 1"
FT Region 69..85
FT /note= "complementarity determining region 1"
FT Region 118..124
FT /note= "complementarity determining region 1"
XX
PN WO200047625-A2.
XX
PD 17-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-US03303.
XX
PR 12-FEB-1999; 99US-0249011.
PR 24-JUN-1999; 99US-0339596.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR WPI; 2000-524532/47.
DR N-PSDB; AAA59696.
XX
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infectious diseases -
XX
PS Example 8; Fig 6A; 162pp; English.
XX
CC The present sequence represents the heavy chain variable region of the
CC murine antibody 1F1. The antibody has a binding specificity to B7
CC molecules. The antibody is used to construct humanized immunoglobulins,
CC which comprise an antigen binding region of non-human origin and a
CC portion of a human immunoglobulin. The humanized immunoglobulins are
CC useful for treating autoimmune diseases, infectious diseases,
CC inflammatory disorders, systemic lupus erythematosus, diabetes
CC mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC also useful for treating a transplant recipient or preventing transplant
CC rejection in a transplant recipient, and treating proliferative disease
CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC thalassemia and aplastic anaemia), inborn errors of metabolism,
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ Sequence 135 AA;

Query Match 77.3%; Score 576.5; DB 21; Length 135;
Best Local Similarity 80.7%; Pred. No. 1.1e-44;
Matches 113; Conservative 6; Mismatches 14; Indels 7; Gaps 1;

Qy 1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
Db 1 mkcswvifflmavvtgvnsevhlqqsgaelvrpgalvklsckpsgfnikdyymhwvkqrp 60

Qy 61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
Db 61 eqglewigwidpengntlydpkfqgkasitadtssntaylqlssltsedtavyycaregl 120

```
Qy    121 YGNYGVYAMDYWGQGTSVTV 140
          :       |||||| |||
Db    121 f-------faywgqgtpvtv 133


RESULT  13
AAR95948
ID   AAR95948 standard; Protein; 137 AA.
XX
AC   AAR95948;
XX
DT   10-FEB-1997  (first entry)
XX
DE   HNK-20 variable heavy chain.
XX
KW   Antibody; HNK-20; variable heavy chain; hybridoma; murine; IgA; mouse;
KW   F glycoprotein; respiratory syncytial virus; RSV; constant region gene;
KW   chimeric antibody; isotype-switched antibody; therapy; infection; human;
KW   pneumonia; bronchiolitis; animal.
XX
OS   Mus musculus.
XX
PN   WO9616974-A1.
XX
PD   06-JUN-1996.
XX
PF   01-DEC-1995;   95WO-US15716.
XX
PR   01-DEC-1994;   94US-0348548.
XX
PA   (ORAV-) ORAVAX INC.
XX
PI   Berdoz J,  Kraehenbuhl J;
XX
DR   WPI; 1996-286826/29.
DR   N-PSDB; AAT30458.
XX
PT   DNA encoding variable region of antibody HNK-20 - for treating
PT   respiratory syncytial virus infection
XX
PS   Claim 15; Fig 5d; 75pp; English.
XX
CC   AAR95946-R95948 represent sequences for variable regions of an antibody
CC   produced by the hybridoma cell line HNK-20.  This sequence represents
CC   the sequence for the antibody HNK-20 variable heavy chain.  HNK-20 is a
CC   murine hybridoma cell line, that produces IgA specific for the F
CC   glycoprotein of respiratory syncytial virus (RSV).  The DNA encoding
CC   these sequences were isolated using primers specific for the 5'
CC   untranslated region of the variable region, and for the intron
CC   downstream of the rearranged J region (see AAT30459-T30545 for primer
CC   sequences). The DNA encoding these sequences can be inserted into vectors
CC   containing heterologous (such as human) constant region genes, for the
CC   production of chimeric and isotype-switched antibodies.  The antibodies
CC   are useful in the treatment and diagnosis of infection by RSV, such as
CC   pneumonia and bronchiolitis, in humans and animals.  By using genomic DNA
CC   as a template, variable region genes can be isolated without producing
CC   fragments that have to be adapted for recombinant antibody expression.
CC   Also, by using the genomic DNA, no knowledge of the DNA sequence
CC   encoding the target variable region is required.  Chimeric antibodies
CC   produced from these proteins, that contain the constant region of the
CC   host being treated, are less likely to cause adverse immune reactions.
XX
SQ   Sequence   137 AA;

  Query Match           76.5%;  Score 570.5;  DB 17;  Length 137;
  Best Local Similarity   81.4%;  Pred. No. 3.8e-44;
  Matches  114;  Conservative    6;  Mismatches   15;  Indels    5;  Gaps    2;

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          ||||||:|||||||||||||||||||||||:||| ||||| |||||||| |:: |||||
Db      1 mkcswvifflmavvtgvnsevqlqqsgaelvrpgalvklsckasgfnikdyymywvkqrp 60

Qy     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
          |||||||| ||| || | |||||||||:||||||||||||||||| |||||||:||   |
Db     61 eqglewigwidpengntvydpkfqgkasitadtssntaylqlsslasedtavyyca---y 117

Qy    121 YGNYGVYAMDYWGQGTSVTV 140
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Db    118 ygt--sywfpywgqgtlvtv 135


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AAR81323
ID   AAR81323 standard; Protein; 123 AA.
XX
AC   AAR81323;
XX
DT   02-APR-1996  (first entry)
XX
DE   Humanized VLA-4 antibody 21.6 heavy chain variable region, Ha.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Claim 11; Page 69; 105pp; English.
XX
CC   The sequence encodes the mouse antibody 21.6 heavy chain variable
CC   region, Ha, directed against leukocyte adhesion molecule VLA-4. Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and AAQ99892) regions
CC   are linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig L chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   for inhibiting adhesion of a leukocyte to an endothelial cell and
CC   for treating inflammatory diseases such as multiple sclerosis.  They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   123 AA;

  Query Match           72.9%;  Score 544;  DB 16;  Length 123;
  Best Local Similarity   82.6%;  Pred. No. 8.2e-42;
  Matches  100;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy     20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
          :||| |||||: |||||||:|| |||||||||||| |:| | | |||:||||||||||||
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```
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          ||||||: ||||||::|||::|||| |||||||:|||||||||||||||||||||| ||
Db     61 dpkfqgrvtitadtsastaymelsslrsedtavyycaregyygnygvyamdywgqgtlvt 120

Qy    140 V 140
          |
Db    121 v 121
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RESULT 15
AAB07969
ID AAB07969 standard; Protein; 135 AA.
XX
AC AAB07969;
XX
DT 14-NOV-2000 (first entry)
XX
DE A heavy chain variable region of humanised 1F1 antibody.
XX
KW Antibody 3D1; B7 molecule; B7; humanised immunoglobulin;
KW autoimmune disease; infectious disease; inflammatory disorder;
KW systemic lupus erythematosus; diabetes mellitus; insulitis; asthma;
KW arthritis; inflammatory bowel disease; cancer; inflammatory dermatitis;
KW multiple sclerosis; transplant rejection; proliferative disease;
KW leukemia; lymphoma; anaemia; sickle-cell anaemia; thalassemia;
KW aplastic anaemia; myeloid dysplasia syndrome.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1..19
FT		/note= "signal peptide"
FT	Protein	20..135
FT		/note= "mature protein"
FT	Region	50..54
FT		/note= "complementarity determining region 1"
FT	Region	69..85
FT		/note= "complementarity determining region 1"
FT	Region	118..124
FT		/note= "complementarity determining region 1"

XX
PN WO200047625-A2.
XX
PD 17-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-US03303.
XX
PR 12-FEB-1999; 99US-0249011.
PR 24-JUN-1999; 99US-0339596.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Co MS, Vasquez M, Carreno B, Celniker AC, Collins M, Goldman S;
PI Gray GS, Knight A, O'hara D, Rup B, Veldman GM;
XX
DR WPI; 2000-524532/47.
DR N-PSDB; AAA59698.
XX
PT Humanized immunoglobulin having a binding specificity to B7-1 (derived
PT from ATCC PTA-263), or B7-2 (derived from ATCC CRL-12524) molecules,
PT modulates immune responses and can therefore treat e.g. autoimmune
PT diseases, infectious diseases -
XX
PS Example 10; Fig 7A; 162pp; English.
XX
CC The present sequence represents the heavy chain variable region of the
CC humanised murine antibody 1F1. The antibody has a binding specificity to
CC B7 molecules. The antibody is used to construct humanized
CC immunoglobulins, which comprise an antigen binding region of non-human
CC origin and a portion of a human immunoglobulin. The humanized
CC immunoglobulins are useful for treating autoimmune diseases, infectious
CC diseases, inflammatory disorders, systemic lupus erythematosus, diabetes
CC mellitus, insulitis, asthma, arthritis, inflammatory bowel disease,
CC inflammatory dermatitis, and multiple sclerosis. The immunoglobulins are
CC also useful for treating a transplant recipient or preventing transplant
CC rejection in a transplant recipient, and treating proliferative disease
CC (leukemia, lymphoma and cancer), anaemia (sickle-cell anaemia,
CC thalassemia and aplastic anaemia), inborn errors of metabolism,
CC congenital immunodeficiency diseases, and myeloid dysplasia syndrome.
XX
SQ Sequence 135 AA;

Query Match 72.3%; Score 539.5; DB 21; Length 135;
Best Local Similarity 75.0%; Pred. No. 2.3e-41;
Matches 105; Conservative 11; Mismatches 17; Indels 7; Gaps 1;

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Db      1 mkcswvifflmavvtgvnsevqlvqsgaevkkpgasvkvsckpsgfnikdyymhwvrqap 60

Qy     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           ||||||| ||| || | |||||||||||||||::|||::|||| |||||||:|||||
Db     61 gqglewigwidpengntlydpkfqgkatitadtststaymelsslrsedtavyycaregl 120

Qy    121 YGNYGVYAMDYWGQGTSVTV 140
          :         |||||| |||
Db    121 f-------faywgqgtlvtv 133
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Search completed: May 7, 2002, 12:22:25
Job time: 246 sec

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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:23:03 ; Search time 32.41 Seconds
(without alignments)
97.206 Million cell updates/sec

Title: US-09-155-739-4
Perfect score: 746
Sequence: 1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	746	100.0	140	2	US-08-561-521-4	Sequence 4, Appli
2	746	100.0	140	5	PCT-US95-01219-4	Sequence 4, Appli
3	645	86.5	123	2	US-08-561-521-9	Sequence 9, Appli
4	645	86.5	123	5	PCT-US95-01219-9	Sequence 9, Appli
5	633	84.9	136	4	US-08-646-265A-29	Sequence 29, Appl
6	595	79.8	136	1	US-08-024-253-2	Sequence 2, Appli
7	593.5	79.6	137	3	US-08-836-561-31	Sequence 31, Appl
8	584	78.3	142	2	US-08-561-521-17	Sequence 17, Appl
9	584	78.3	142	5	PCT-US95-01219-17	Sequence 17, Appl
10	562	75.3	125	2	US-08-561-521-44	Sequence 44, Appl
11	562	75.3	125	5	PCT-US95-01219-44	Sequence 44, Appl
12	554	74.3	136	4	US-08-348-548-8	Sequence 8, Appli
13	554	74.3	136	5	PCT-US95-15716-8	Sequence 8, Appli
14	544	72.9	123	2	US-08-561-521-11	Sequence 11, Appl
15	544	72.9	123	5	PCT-US95-01219-11	Sequence 11, Appl
16	528.5	70.8	120	2	US-07-934-373C-6	Sequence 6, Appli
17	528.5	70.8	120	3	US-08-437-642B-6	Sequence 6, Appli
18	528.5	70.8	120	5	PCT-US93-07832-6	Sequence 6, Appli
19	516	69.2	121	2	US-08-822-830B-2	Sequence 2, Appli
20	513	68.8	121	2	US-08-822-830B-13	Sequence 13, Appl
21	511	68.5	120	2	US-08-950-660-2	Sequence 2, Appli
22	511	68.5	120	5	PCT-US93-00030-2	Sequence 2, Appli
23	511	68.5	120	5	PCT-US93-00924-2	Sequence 2, Appli
24	505.5	67.8	138	3	US-08-603-024-2	Sequence 2, Appli
25	505.5	67.8	139	1	US-08-253-877C-8	Sequence 8, Appli
26	505.5	67.8	139	2	US-08-452-164A-8	Sequence 8, Appli
27	504	67.6	254	2	US-08-792-824-4	Sequence 4, Appli
28	504	67.6	254	2	US-08-792-824-7	Sequence 7, Appli
29	504	67.6	254	2	US-08-792-824-10	Sequence 10, Appl
30	504	67.6	254	2	US-08-792-824-13	Sequence 13, Appl
31	502	67.3	136	4	US-08-646-265A-99	Sequence 99, Appl
32	500.5	67.1	118	2	US-08-232-081B-38	Sequence 38, Appl
33	498.5	66.8	113	1	US-08-207-169A-2	Sequence 2, Appli
34	494.5	66.3	118	3	US-08-767-128-22	Sequence 22, Appl
35	488.5	65.5	255	4	US-09-171-945-19	Sequence 19, Appl
36	483.5	64.8	139	2	US-08-182-067-10	Sequence 10, Appl
37	483.5	64.8	139	2	US-08-465-313-10	Sequence 10, Appl
38	482.5	64.7	139	2	US-08-039-198B-10	Sequence 10, Appl
39	475.5	63.7	137	1	US-08-477-877B-86	Sequence 86, Appl
40	475.5	63.7	137	2	US-08-472-281A-86	Sequence 86, Appl
41	475.5	63.7	137	2	US-08-477-989B-86	Sequence 86, Appl
42	475	63.7	117	2	US-08-290-592E-18	Sequence 18, Appl
43	475	63.7	117	5	PCT-US95-10053-15	Sequence 15, Appl
44	475	63.7	117	5	PCT-US96-09448-18	Sequence 18, Appl
45	473.5	63.5	153	4	US-09-096-244-4	Sequence 4, Appli

ALIGNMENTS

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RESULT   1
US-08-561-521-4
; Sequence 4, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  140 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-4


  Query Match             100.0%;  Score 746;  DB 2;  Length 140;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-68;
  Matches  140;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
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Db      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           ||||||||||||||||||||
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RESULT   2
PCT-US95-01219-4
; Sequence 4, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  140 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-4


  Query Match             100.0%;  Score 746;  DB 5;  Length 140;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-68;
  Matches  140;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT   3
US-08-561-521-9
; Sequence 9, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-9


  Query Match             86.5%;  Score 645;  DB 2;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-58;
  Matches  121;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db     121 V 121


RESULT   4
PCT-US95-01219-9
; Sequence 9, Application PC/TUS9501219
;  GENERAL INFORMATION:
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;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-9


  Query Match             86.5%;  Score 645;  DB 5;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-58;
  Matches  121;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 120

Qy     140 V 140
           |
Db     121 V 121


RESULT   5
US-08-646-265A-29
; Sequence 29, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  136 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-29


  Query Match             84.9%;  Score 633;  DB 4;  Length 136;
  Best Local Similarity   89.3%;  Pred. No. 4.1e-57;
  Matches  125;  Conservative    2;  Mismatches    7;  Indels    6;  Gaps    2;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHWAKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||||||||:| ||||||||||||||||||||||||||||||||||:||   |
Db      61 EQGLEWIGRIDPADGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCA-SAY 119

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           | |     ||||||||||||
Db     120 YVN-----QDYWGQGTSVTV 134


RESULT   6
US-08-024-253-2
; Sequence 2, Application US/08024253
; Patent No. 5785968
;  GENERAL INFORMATION:
;    APPLICANT:  KIMACHI, Kazuhiko
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  NISHIYAMA, Kiyoto
;    APPLICANT:  TOKIYOSHI, Sachio
;    APPLICANT:  TOHYA, Yukinobu
;    APPLICANT:  MIKAMI, Takeshi
;    TITLE OF INVENTION:  ANTI-FELINE CALCIVIRUS RECOMBINANT
;    TITLE OF INVENTION:  ANTIBODY AND GENE FRAGMENT ENCODING THE SAME
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WEGNER, CANTOR, MUELLER & PLAYER
;      STREET:  1233 20th Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
```

```
;       COUNTRY:  U.S.A.
;       ZIP:  20036-8218
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/024,253
;       FILING DATE:  19930301
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 79189/1992
;       FILING DATE:  28-FEB-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  CANTOR, Herbert I.
;       REGISTRATION NUMBER:  24,392
;       REFERENCE/DOCKET NUMBER:  P-500-23744
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202) 887-0400
;       TELEFAX:  (202) 835-0605
;       TELEX:  440706 WEGBR
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  136 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-024-253-2


  Query Match             79.8%;  Score 595;  DB 1;  Length 136;
  Best Local Similarity   82.9%;  Pred. No. 3e-53;
  Matches  116;  Conservative    8;  Mismatches   10;  Indels    6;  Gaps    1;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |||||||:|||||||||||||||||||||||||||||||:|||||||||||||||:| |||||
Db       1 MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVKPGASVRLSCTASGFNIKDTYMHWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||||||||||| |||||:|||||||||||| |||||::|||||||||||:|| |
Db      61 EQGLEWIGRIDPANGNTKYDPRFQGKATITADTSFNTAYLQVNSLTSEDTAVYYCASGGN 120

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
                 : |||||| |||
Db     121 AW------LAYWGQGTLVTV 134


RESULT   7
US-08-836-561-31
; Sequence 31, Application US/08836561
; Patent No. 6018032
;  GENERAL INFORMATION:
;    APPLICANT:  KOIKE, Masamichi
;    APPLICANT:  FURUYA, Akiko
;    APPLICANT:  NAKAMURA, Kazuyasu
;    APPLICANT:  IIDA, Akihiro
;    APPLICANT:  ANAZAWA, Hideharu
;    APPLICANT:  HANAI, No. 6018032uo
;    APPLICANT:  TAKATSU, Kiyoshi
;    TITLE OF INVENTION:  Antibody Against Human Interleukin-5
;    TITLE OF INVENTION:  Receptor Alpha Chain
;    NUMBER OF SEQUENCES:  106
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds LLP
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/836,561
;      FILING DATE:  09-MAY-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 232384/95
;      FILING DATE:  11-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lawrence, III, Stanton T
;      REGISTRATION NUMBER:  25,736
;      REFERENCE/DOCKET NUMBER:  7005-115-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-790-9090
;      TELEFAX:  212-869-9741
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  137 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-836-561-31


  Query Match             79.6%;  Score 593.5;  DB 3;  Length 137;
  Best Local Similarity   82.9%;  Pred. No. 4.2e-53;
  Matches  116;  Conservative    6;  Mismatches   13;  Indels    5;  Gaps    1;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||:|||||||||||||||||||||||||||||| ||||||||||||||:| |||||
Db       1 MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVKPGASVNLSCTASGFNIKDTYMHWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||||||||||| || ||||| |||| |||||||||||||||||||||:|
Db      61 EQGLEWIGRIDPANGNTKSDPKFQAKATIAADTSSNTAYLQLSSLTSEDTAVYYCT---- 116

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
             |   :   |||||||::||
Db     117 -GGLRLRFFDYWGQGTTLTV 135


RESULT   8
US-08-561-521-17
; Sequence 17, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
```

```
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  142 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-17


  Query Match             78.3%;  Score 584;  DB 2;  Length 142;
  Best Local Similarity   77.1%;  Pred. No. 4.1e-52;
  Matches  108;  Conservative   15;  Mismatches   17;  Indels    0;  Gaps    0;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |  :| :| |:||  | :|:||| ||||| |||||||:|| |||||||||||| |:| |
Db       1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
             | |||:||||||||||||||||||: |||||||::|||::|||| |||||||:||||||
Db      61 GQRLEWMGRIDPANGYTKYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY 120

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           ||||||||||||||| |||
Db     121 YGNYGVYAMDYWGQGTLVTV 140


RESULT  9
PCT-US95-01219-17
; Sequence 17, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  142 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-17


  Query Match             78.3%;  Score 584;  DB 5;  Length 142;
  Best Local Similarity   77.1%;  Pred. No. 4.1e-52;
  Matches  108;  Conservative   15;  Mismatches   17;  Indels    0;  Gaps    0;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |  :| :| |:||  | :|:||| ||||| |||||||:|| |||||||||||| |:| |
Db       1 MDWTWRVFCLLAVAPGAHSQVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
             | |||:||||||||||||||||||: |||||||::|||::|||| |||||||:||||||
Db      61 GQRLEWMGRIDPANGYTKYDPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGY 120

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           ||||||||||||||| |||
Db     121 YGNYGVYAMDYWGQGTLVTV 140


RESULT  10
US-08-561-521-44
; Sequence 44, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  125 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-44
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  Query Match            75.3%;  Score 562;  DB 2;  Length 125;
  Best Local Similarity  89.4%;  Pred. No. 5.9e-50;
  Matches  110;  Conservative    2;  Mismatches    9;  Indels    2;  Gaps    1;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           |||||||||||||||||||||||||||||||:| |||||||||||||||||||| |||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYY--GNYGVYAMDYWGQGTS 137
           |||||||||||||||||||||||||||||||:|||  ||     | ||||||||||
Db      61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARGYYYYDSXVGYYAMDYWGQGTX 120

Qy     138 VTV 140
          |||
Db     121 VTV 123


RESULT  11
PCT-US95-01219-44
; Sequence 44, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  125 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-44


  Query Match            75.3%;  Score 562;  DB 5;  Length 125;
  Best Local Similarity  89.4%;  Pred. No. 5.9e-50;
  Matches  110;  Conservative    2;  Mismatches    9;  Indels    2;  Gaps    1;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           |||||||||||||||||||||||||||||||:| |||||||||||||||||||| |||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYY--GNYGVYAMDYWGQGTS 137
           |||||||||||||||||||||||||||||||:|||  ||     | ||||||||||
Db      61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARGYYYYDSXVGYYAMDYWGQGTX 120

Qy     138 VTV 140
          |||
Db     121 VTV 123


RESULT  12
US-08-348-548-8
; Sequence 8, Application US/08348548
; Patent No. 6258529
;  GENERAL INFORMATION:
;    APPLICANT:  Berdoz, Jose
;    APPLICANT:  Kraehenbuhl, Jean Pierre
;    TITLE OF INVENTION:  PCR AMPLIFICATION OF REARRANGED GENOMIC
;    TITLE OF INVENTION:  VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
;    NUMBER OF SEQUENCES:  108
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street, Suite 3100
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/348,548
;      FILING DATE:  01-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  06132/009001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-5070
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  136 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-348-548-8


  Query Match            74.3%;  Score 554;  DB 4;  Length 136;
  Best Local Similarity  80.7%;  Pred. No. 4.3e-49;
  Matches  113;  Conservative    6;  Mismatches   15;  Indels    6;  Gaps    3;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||:|||||||| |||||||||||||||:||| ||||| |||||||| |:: |||||
Db       1 MKCSWVIFFLMAVVT-VNSEVQLQQSGAELVRPGALVKLSCKASGFNIKDYYMYWVKQRP 59

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||| ||| || | |||||||||:|||||||||||||||| |||||||:||   |
Db      60 EQGLEWIGWIDPENGNTVYDPKFQGKASITADTSSNTAYLQLSSLASEDTAVYYCA---Y 116

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           ||    |   |||||| |||
Db     117 YGT--SYWFPYWGQGTLVTV 134


RESULT  13
PCT-US95-15716-8
; Sequence 8, Application PC/TUS9515716
;  GENERAL INFORMATION:
;    APPLICANT:  Berdoz, Jose
```

```
;    APPLICANT:  Kraehenbuhl, Jean Pierre
;    TITLE OF INVENTION:  PCR AMPLIFICATION OF REARRANGED GENOMIC
;    TITLE OF INVENTION:  VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
;    NUMBER OF SEQUENCES:  108
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson
;      STREET:  225 Franklin Street, Suite 3100
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30B
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/15716
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/348,548
;      FILING DATE:  01-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clark, Paul T.
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  06132/009001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-5070
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  136 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-15716-8


  Query Match             74.3%;  Score 554;  DB 5;  Length 136;
  Best Local Similarity   80.7%;  Pred. No. 4.3e-49;
  Matches  113;  Conservative    6;  Mismatches   15;  Indels    6;  Gaps    3;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||:|||||||| |||||||||||||||:||| ||||| |||||||| |:: |||||
Db       1 MKCSWVIFFLMAVVT-VNSEVQLQQSGAELVRPGALVKLSCKASGFNIKDYYMYWVKQRP 59

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||| ||| || | |||||||||:|||||||||||||||| |||||||:||   |
Db      60 EQGLEWIGWIDPENGNTVYDPKFQGKASITADTSSNTAYLQLSSLASEDTAVYYCA---Y 116

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           ||    |   |||||| |||
Db     117 YGT--SYWFPYWGQGTLVTV 134


RESULT  14
US-08-561-521-11
; Sequence 11, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-11


  Query Match             72.9%;  Score 544;  DB 2;  Length 123;
  Best Local Similarity   82.6%;  Pred. No. 3.9e-48;
  Matches  100;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           :||| ||||: |||||||:|| |||||||||||| |:| | | |||:||||||||||||
Db       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
           ||||||: |||||||::|||::|||| |||||||:||||||||||||||||||||| ||
Db      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Qy     140 V 140
           |
Db     121 V 121


RESULT  15
PCT-US95-01219-11
; Sequence 11, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  PCT/US95/01219
;       FILING DATE:  25-JAN-1995
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/186,269
;       FILING DATE:  25-JAN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William L.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  15270-14
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-543-9600
;       TELEFAX:  415-543-5043
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  123 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US95-01219-11


  Query Match             72.9%;  Score 544;  DB 5;  Length 123;
  Best Local Similarity   82.6%;  Pred. No. 3.9e-48;
  Matches  100;  Conservative   11;  Mismatches   10;  Indels    0;  Gaps    0;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           :||| ||||| |||||||:|| |||||||||||| |:| | | |||:|||||||||||||
Db       1 QVQLVQSGAEVKKPGASVKVSCKASGFNIKDTYIHWVRQAPGQRLEWMGRIDPANGYTKY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
           |||||| ||||||| ::||| ::|||| ||||||| ||||||||||||||||||||||| ||
Db      61 DPKFQGRVTITADTSASTAYMELSSLRSEDTAVYYCAREGYYGNYGVYAMDYWGQGTLVT 120

Qy     140 V 140
           |
Db     121 V 121


Search completed: May  7, 2002, 12:23:04
Job time: 175 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:23:47 ; Search time 37.68 Seconds
(without alignments)
283.026 Million cell updates/sec

Title: US-09-155-739-4
Perfect score: 746
Sequence: 1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	603.5	80.9	178	2	S29594	Ig gamma chain (WM
2	597	80.0	136	2	S04576	Ig heavy chain pre
3	570.5	76.5	137	2	S52445	Ig heavy chain V r
4	567.5	76.1	123	2	PH1403	Ig heavy chain V r
5	539	72.3	120	2	S03471	Ig heavy chain V-D
6	523	70.1	117	2	S17586	Ig heavy chain V r
7	521.5	69.9	122	2	S06823	Ig heavy chain V r
8	515	69.0	115	2	S03482	Ig heavy chain V-D
9	500	67.0	116	2	S24289	Ig gamma chain V r
10	498	66.8	120	2	S03484	Ig heavy chain V-D
11	494.5	66.3	268	2	A56446	Ig heavy chain V r
12	493.5	66.2	108	2	PH1012	Ig heavy chain V r
13	492	66.0	221	2	S49220	Ig gamma-1 chain -
14	472.5	63.3	114	4	A47271	nitrophenyl phosph
15	471	63.1	140	2	PH1482	Ig heavy chain V r
16	467	62.6	107	2	PH1013	Ig heavy chain V r
17	466.5	62.5	139	2	PS0024	Ig heavy chain pre
18	464.5	62.3	139	1	MHMS18	Ig heavy chain pre
19	462.5	62.0	99	2	D37262	Ig heavy chain V r
20	461.5	61.9	115	2	PL0246	Ig heavy chain V r
21	461.5	61.9	139	2	A27609	Ig heavy chain pre
22	460.5	61.7	141	2	JL0076	Ig heavy chain pre
23	459	61.5	135	2	PH1492	Ig heavy chain V r
24	459	61.5	140	1	HVMSG7	Ig heavy chain pre
25	457.5	61.3	107	2	A27646	Ig heavy chain V r
26	457	61.3	138	2	E32513	Ig heavy chain pre
27	456	61.1	249	2	S41374	single chain Fv an
28	455.5	61.1	141	2	A39276	Ig heavy chain pre
29	455	61.0	140	2	PH1498	Ig heavy chain V r
30	454.5	60.9	133	2	PC1155	Ig heavy chain pre
31	454	60.9	118	2	S25174	Ig heavy chain V r
32	454	60.9	138	2	S21810	Ig heavy chain V r
33	453	60.7	140	2	PH1484	Ig heavy chain V r
34	452	60.6	135	2	PH1493	Ig heavy chain V r
35	451.5	60.5	469	2	S37483	Ig gamma-2a chain
36	451	60.5	135	2	PH1494	Ig heavy chain V r
37	447	59.9	140	2	PH1489	Ig heavy chain V r
38	444	59.5	140	2	PH1486	Ig heavy chain V r
39	441	59.1	140	2	PH1488	Ig heavy chain V r
40	440.5	59.0	120	2	S41394	Ig heavy chain V r
41	440	59.0	122	2	S20643	Ig heavy chain V r
42	440	59.0	246	2	S38950	Ig gamma chain - m
43	440	59.0	446	2	S40295	Ig gamma-2a chain
44	439	58.8	123	2	S20646	Ig heavy chain V r
45	438	58.7	99	2	C37262	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S29594
Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S29594
R;Seymour, R.
submitted to the EMBL Data Library, February 1991
A;Reference number: S29593
A;Accession: S29594
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <SEY>
A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C;Keywords: immunoglobulin

Query Match 80.9%; Score 603.5; DB 2; Length 178;
Best Local Similarity 88.1%; Pred. No. 1.5e-45;
Matches 118; Conservative 6; Mismatches 5; Indels 5; Gaps 2;

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Qy       7 MFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEW 66
           :|||||||||||||||||||||||||||||||||||||||||||||:| |||||:|||||
Db       1 IFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEW 60

Qy      67 IGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGV 126
           ||||||||||:||||||||||||||:|||||||||||||||||:|      |||
Db      61 IGRIDPANGYTEYDPKFQGKATITADTSTNTAYLQLSSLTSEDTAVYYCTG----GNY-A 115

Qy     127 YAMDYWGQGTSVTV 140
           | ||||||||||||
Db     116 YGMDYWGQGTSVTV 129
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RESULT 2
S04576
Ig heavy chain precursor V region (MRL-histone 7H) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000
C;Accession: S04576
R;Kofler, R.; Noonan, D.J.; Strohal, R.; Balderas, R.S.; Moller, N.P.H.; Dixon, F.J.;
Eur. J. Immunol. 17, 91-95, 1987
A;Title: Molecular analysis of the murine lupus-associated anti-self response: involv
A;Reference number: S04573; MUID:87133856
A;Accession: S04576
A;Molecule type: mRNA
A;Residues: 1-136 <KOF>
A;Cross-references: EMBL:X14624; NID:g52029; PIDN:CAA32777.1; PID:g52030
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-136/Product: Ig heavy chain V region (fragment) #status predicted <MAT>

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 597; DB 2; Length 136;
Best Local Similarity 82.9%; Pred. No. 4.1e-45;
Matches 116; Conservative 6; Mismatches 12; Indels 6; Gaps 1;

```
Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |||||||:|||||||  ||||||||||||||||:||||||||||||||||||  |:|  |||||
Db       1 MKCSWVIFFLMAVVIGVNSEVQLQQSGAELVRPGASVKLSCTASGFNIKDDYMHWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           ||||||||  |||  ||  |:|  |||||||:||||||| ||||||||||||||:|
Db      61 EQGLEWIGWIDPENGDTQYASKFQGKATMTADTSSNTTYLQLSSLTSEDTAVYYCT---- 116

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
              || ||||||||||||||
Db     117 --TYGAYAMDYWGQGTSVTV 134
```

RESULT 3
S52445
Ig heavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52445
R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged ger
A;Reference number: S52445
A;Accession: S52445
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-137 <BER>
A;Cross-references: EMBL:X82690; NID:g673439; PIDN:CAA58011.1; PID:g673440
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-115/Domain: immunoglobulin homology <IMM>

Query Match 76.5%; Score 570.5; DB 2; Length 137;
Best Local Similarity 81.4%; Pred. No. 8.4e-43;
Matches 114; Conservative 6; Mismatches 15; Indels 5; Gaps 2;

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Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||:|||||||||||||||||||||||:||| ||||| |||||||| |:: |||||
Db       1 MKCSWVIFFLMAVVTGVNSEVQLQQSGAELVRPGALVKLSCKASGFNIKDYYMYWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           ||||||||  ||| ||  |  |||||||||:|||||||||||||||| |||||||:||   |
Db      61 EQGLEWIGWIDPENGNTVYDPKFQGKASITADTSSNTAYLQLSSLASEDTAVYYCA---Y 117

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           ||    |   |||||| |||
Db     118 YGT--SYWFPYWGQGTLVTV 135
```

RESULT 4
PH1403
Ig heavy chain V region (clone micro m- 46-6, 46-12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C;Accession: PH1403
R;Shirasawa, T.; Miyazoe, I.; Hagiwara, S.; Kimoto, H.; Shigemoto, K.; Taniguchi, M.; Ta
J. Exp. Med. 176, 1209-1214, 1992
A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
ia virus.
A;Reference number: PH1403; MUID:93018837
A;Accession: PH1403
A;Molecule type: DNA
A;Residues: 1-123 <SHI>
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-118/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 567.5; DB 2; Length 123;
Best Local Similarity 94.9%; Pred. No. 1.4e-42;
Matches 111; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

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Qy       1 MKCSWVMFFLMAVVT-GVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQR 59
           ||||||:|||||||| ||||||||||||||||||||||||||||||||||:| ||||
Db       1 MKCSWVIFFLMAVVTAGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQR 60

Qy      60 PEQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCA 116
           |||||||||||||||| ||||||||||||||||||||||||||||||||||:||
Db      61 PEQGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCA 117
```

RESULT 5
S03471
Ig heavy chain V-D-J region (hybridoma G5 Bb 2.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S03471; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
hypervariable regions.
A;Reference number: S03471; MUID:84057768
A;Accession: S03471
A;Molecule type: mRNA
A;Residues: 7-120 <ROC1>
A;Cross-references: EMBL:X01820; NID:g51833; PIDN:CAA25962.1; PID:g1333983
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.3%; Score 539; DB 2; Length 120;
Best Local Similarity 89.3%; Pred. No. 4e-40;
Matches 108; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

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Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           ||||||||||||||||||||||||||||||:| |||||||||||||||||| |||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
           |||||||||||||||||||||||||||||:|||    |     ||||||||||||
Db      61 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR----GWLRRDAMDYWGQGTSVT 116

Qy     140 V 140
           |
Db     117 V 117
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RESULT 6
S17586
Ig heavy chain V region (E8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S17586
R;Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.
J. Mol. Biol. 221, 455-462, 1991

```
A;Title: Biochemical implications from the variable gene sequences of an anti-cytochrome
  forms.
A;Reference number: S17586; MUID:92015240
A;Accession: S17586
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <MYL>
A;Cross-references: EMBL:X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match             70.1%;  Score 523;  DB 2;  Length 117;
  Best Local Similarity   85.2%;  Pred. No. 9.6e-39;
  Matches  104;  Conservative    7;  Mismatches    3;  Indels    8;  Gaps    3;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           |||||||||||||||||||||||||||||||:| ||||||:||||||||||:| |||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEKGLEWIGRIDPASGNTKY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY-YGNYGVYAMDYWGQGTSV 138
           ||||| |||||||||||||||||||||||:||  || |||:     |||||||::
Db      61 DPKFQDKATITADTSSNTAYLQLSSLTSEDTAVYYCA--GYDYGNF-----DYWGQGTTL 113

Qy     139 TV 140
           ||
Db     114 TV 115


RESULT   7
S06823
Ig heavy chain V region (clone IIc) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06823
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531
A;Accession: S06823
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-122 <MIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>


  Query Match             69.9%;  Score 521.5;  DB 2;  Length 122;
  Best Local Similarity   86.9%;  Pred. No. 1.4e-38;
  Matches  106;  Conservative    4;  Mismatches    9;  Indels    3;  Gaps    3;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIH-CVKQRPEQGLEWIGRIDPANGYTK 78
           |||||||||||||||||||||||||||||||:|  ||||||||||||||||||| ||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHEWVKQRPEQGLEWIGRIDPANGNTK 60

Qy      79 YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSV 138
           |||||||||||||||||||||||||||||||:||| |:        :|||||||||
Db      61 YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCAR-GWL-RRDAMGVDYWGQGTSV 118

Qy     139 TV 140
           ||
Db     119 TV 120


RESULT   8
S03482
Ig heavy chain V-D-J region (hybridoma G8 Ad 3.8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03482; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau,
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-
hypervariable regions.
A;Reference number: S03471; MUID:84057768
A;Accession: S03482
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-115 <ROC1>
A;Cross-references: EMBL:X03219
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Foug
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>


  Query Match             69.0%;  Score 515;  DB 2;  Length 115;
  Best Local Similarity   83.5%;  Pred. No. 4.7e-38;
  Matches  101;  Conservative    4;  Mismatches   10;  Indels    6;  Gaps    1;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           |||||||||||||||||||||||||||||||:| |||||||||||||||| | |||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPAKGNTKY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
           |||||||||| |||||||||| |||||||||||:|||    |       |||||||::|
Db      61 DPKFQGKATITTDTSSNTAYLQFSSLTSEDTAVYYCARGTTVGR------DYWGQGTTLT 114

Qy     140 V 140
           |
Db     115 V 115


RESULT   9
S24289
Ig gamma chain V region (JS34/32) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S24289
R;Moncharmont, B.
submitted to the EMBL Data Library, September 1991
A;Description: Cloning and sequencing of the cDNA coding for the variable regions of
A;Reference number: S24287
A;Accession: S24289
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MON>
A;Cross-references: EMBL:X62705; NID:g51690; PIDN:CAA44584.1; PID:g1333963
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>


  Query Match             67.0%;  Score 500;  DB 2;  Length 116;
  Best Local Similarity   81.0%;  Pred. No. 9.5e-37;
  Matches   98;  Conservative    9;  Mismatches    6;  Indels    8;  Gaps    2;

Qy      21 VQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYD 80
           ||||:||||||||||||||||| |||:|||:| |:|||:|||||||||||||| | :|
Db       1 VQLQESGAELVKPGASVKLSCTASVFNIQDTYMHWVRQRPKQGLEWIGRIDPANGNTHFD 60

Qy      81 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-EGYYGNYGVYAMDYWGQGTSVT 139
           |||||||||||||||||||||||||||||||||:|||  |||        |||||||::|
Db      61 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARWAGYY-------FDYWGQGTTLT 113

Qy     140 V 140
```

```
Db    114 V 114
```

RESULT 10
S03484
Ig heavy chain V-D-J region (hybridoma G7 Ab 2.9) - mouse (fragment)
C;Species: Mus musculus (house mouse)
A;Variety: strain BALB/c
C;Date: 26-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 21-Jan-2000
C;Accession: S03484; S07453
R;Rocca-Serra, J.; Matthes, H.W.; Kaartinen, M.; Milstein, C.; Theze, J.; Fougereau, M.
EMBO J. 2, 867-872, 1983
A;Title: Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of four anti-GAT
hypervariable regions.
A;Reference number: S03471; MUID:84057768
A;Accession: S03484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 10-120 <ROC1>
A;Cross-references: EMBL:X07144
A;Note: this sequence was determined from the differentiated gene
R;Rocca-Serra, J.; Mazie, J.C.; Moinier, D.; Leclercq, L.; Somme, G.; Theze, J.; Fougere
J. Immunol. 129, 2554-2558, 1982
A;Title: The limited diversity of the mouse gamma-chains anti-GAT repertoire does not se
A;Reference number: S07453; MUID:83058021
A;Accession: S07453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-43 <ROC2>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.8%; Score 498; DB 2; Length 120;
Best Local Similarity 82.6%; Pred. No. 1.5e-36;
Matches 100; Conservative 5; Mismatches 12; Indels 4; Gaps 1;

```
Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           ||||||||||||||||||||||||||||||||||:| ||||||||||||||||||  :||
Db       1 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANXNSKY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
            ||||| |||||||||: |||||||||| |||||:| |    | :   ||||||||||||
Db      61 GPKFQGXATITADTSSSAAYLQLSSLTSGDTAVYYCTR----GWFRRDAMDYWGQGTSVT 116

Qy     140 V 140
          |
Db     117 V 117
```

RESULT 11
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identi
A;Reference number: A56446; MUID:95229583
A;Accession: A56446
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 <TAN>
A;Cross-references: GB:U20617
C;Keywords: heterotetramer; immunoglobulin

Query Match 66.3%; Score 494.5; DB 2; Length 268;
Best Local Similarity 80.3%; Pred. No. 6.8e-36;
Matches 98; Conservative 8; Mismatches 11; Indels 5; Gaps 2;

```
Qy      19 SEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTK 78
           ::|:||:|||||||||||||||| |||||||||:| ||||||||||||| |||| ||
Db       2 AQVKLQESGAELVKPGASVKLSCTTSGFNIKDTYMHWVKQRPEQGLEWIGRIAPANGITK 61

Qy      79 YDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSV 138
           |||||||||| |||||||||||||||||||||:||   |   |     :|||||:|
Db      62 YDPKFQGKATIAADTSSNTAYLQLSSLTSEDTAVYYCA-SYYLTRY----ENYWGQGTTV 116

Qy     139 TV 140
           ||
Db     117 TV 118
```

RESULT 12
PH1012
Ig heavy chain V region (clone 17p.73) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1012
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PH0971; MUID:92381444
A;Accession: PH1012
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-108 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.2%; Score 493.5; DB 2; Length 108;
Best Local Similarity 85.8%; Pred. No. 3.3e-36;
Matches 97; Conservative 3; Mismatches 8; Indels 5; Gaps 1;

```
Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           ||||||||||||:|||||||||||||||||| |:| |||||||||||||||||| |||
Db       1 EVQLQQSGAELVRPGASVKLSCTASGFNIKDDYMHWVKQRPEQGLEWIGRIDPANGNTKY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYW 132
           |||| |||||||||||||||||||||||||:|||   |     ||||||
Db      61 APKFQDKATITADTSSNTAYLQLSSLTSEDTAVYYCARRDNY-----YAMDYW 108
```

RESULT 13
S49220
Ig gamma-1 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C;Accession: S49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A;Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing
A;Reference number: S49220
A;Accession: S49220
A;Molecule type: mRNA
A;Residues: 1-221 <KIP>
A;Cross-references: EMBL:Z37502; NID:g541778; PIDN:CAA85732.1; PID:g541779
A;Experimental source: strain Balb/c
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-120/Domain: V region #status predicted <VRG>
F;121-221/Domain: C region #status predicted <CRG>
F;139-203/Domain: immunoglobulin homology <IMM>

Query Match 66.0%; Score 492; DB 2; Length 221;
Best Local Similarity 79.3%; Pred. No. 9.2e-36;
Matches 96; Conservative 8; Mismatches 13; Indels 4; Gaps 1;

```
Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
```

```
          ::|:| :|||||||| ||||||||||||||||||||:| ||||||||||||||||||||  ||
Db      1 QVKLLESGAELVKSGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGEIKY 60

Qy     80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
          |||||| |||||||:|||||||||||||||||:| | |    ||     ||||||::|
Db     61 DPKFQGTATITADTSTNTAYLQLSSLTSEDTAVYYCVRRG----YGSSQEPYWGQGTTLT 116

Qy    140 V 140
          |
Db    117 V 117
```

RESULT 14
A47271
nitrophenyl phosphonate-specific antibody 48G7 heavy chain VDJ - synthetic (fragment)
C;Species: synthetic
A;Note: Mus musculus (house mouse) gene engineered and expressed in Escherichia coli
C;Date: 21-Sep-1993 #sequence_revision 11-Aug-1995 #text_change 11-Aug-1995
C;Accession: A47271
R;Lesley, S.A.; Patten, P.A.; Schultz, P.G.
Proc. Natl. Acad. Sci. U.S.A. 90, 1160-1165, 1993
A;Title: A genetic approach to the generation of antibodies with enhanced catalytic acti
A;Reference number: A47271; MUID:93165660
A;Accession: A47271
A;Molecule type: DNA; protein
A;Residues: 1-114 <LES>
A;Note: sequence extracted from NCBI backbone (NCBIN:124854, NCBIP:124855)
A;Note: parts of this sequence were determined by protein sequencing
F;22-96/Disulfide bonds: #status predicted

```
  Query Match             63.3%;  Score 472.5;  DB 4;  Length 114;
  Best Local Similarity   77.7%;  Pred. No. 2.3e-34;
  Matches   94;  Conservative    8;  Mismatches   10;  Indels    9;  Gaps    2;

Qy     20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
          :|:| :|||||||||||||||||||||||||:| |||||:|||||||||||||  |||
Db      1 QVKLLESGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEWIGRIDPANVDTKY 60

Qy     80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
          ||||| |||||||||| | ||||| |||||||||:||   |||        ||||||::|
Db     61 DPKFQDKATITADTSSKTTYLQLSGLTSEDTAVYYCA--SYYG-------IYWGQGTTLT 111

Qy    140 V 140
          |
Db    112 V 112
```

RESULT 15
PH1482
Ig heavy chain V region (clones 36-35[TG] and X7-TG) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: PH1482; PH1495
R;Giusti, A.M.; Manser, T.
J. Exp. Med. 177, 797-809, 1993
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that hav
d for somatic mutation.
A;Reference number: PH1482; MUID:93171820
A;Accession: PH1482
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-140 <GIU>
A;Experimental source: hybridoma cell
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

```
  Query Match             63.1%;  Score 471;  DB 2;  Length 140;
  Best Local Similarity   65.0%;  Pred. No. 3.8e-34;
  Matches   91;  Conservative   19;  Mismatches   28;  Indels    2;  Gaps    1;

Qy      1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
          |  |::  ||::|  ||:|||||||||||||: |:||||:|| |||:       |: |||||
Db      1 MGWSFIFLFLLSVTAGVHSEVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRP 60

Qy     61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           ||||||| |:| |||||||: ||:|| |:| | ||:|||:|| |||||||:|||||||  |
Db     61 GQGLEWIGYINPGNGYTKYNEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVY 120

Qy    121 YGNYGVYAMDYWGQGTSVTV 140
          ||  | |  |||||||::||
Db    121 YG--GSYYFDYWGQGTTLTV 138
```

Search completed: May 7, 2002, 12:23:47
Job time: 198 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:32:34 ; Search time 21.92 Seconds
(without alignments)
234.173 Million cell updates/sec

Title: US-09-155-739-4
Perfect score: 746
Sequence: 1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	464.5	62.3	139	1	HV07_MOUSE	P01751 mus musculu
2	459	61.5	140	1	HV02_MOUSE	P01746 mus musculu
3	425	57.0	120	1	HV03_MOUSE	P01747 mus musculu
4	422.5	56.6	137	1	HV11_MOUSE	P01755 mus musculu
5	416	55.8	138	1	HV48_MOUSE	P03980 mus musculu
6	411	55.1	117	1	HV09_MOUSE	P01753 mus musculu
7	396	53.1	136	1	HV15_MOUSE	P01759 mus musculu
8	393	52.7	117	1	HV06_MOUSE	P01750 mus musculu
9	393	52.7	117	1	HV49_MOUSE	P06328 mus musculu
10	389	52.1	117	1	HV10_MOUSE	P01754 mus musculu
11	388	52.0	117	1	HV04_MOUSE	P01748 mus musculu
12	381	51.1	117	1	HV52_MOUSE	P06327 mus musculu
13	379	50.8	117	1	HV13_MOUSE	P01757 mus musculu
14	379	50.8	121	1	HV01_MOUSE	P01745 mus musculu
15	378.5	50.7	147	1	HV1C_HUMAN	P01744 homo sapien
16	374	50.1	117	1	HV05_MOUSE	P01749 mus musculu
17	374	50.1	117	1	HV12_MOUSE	P01756 mus musculu
18	372	49.9	117	1	HV14_MOUSE	P01758 mus musculu
19	368.5	49.4	118	1	HV51_MOUSE	P06330 mus musculu
20	367	49.2	117	1	HV1B_HUMAN	P01743 homo sapien
21	360.5	48.3	120	1	HV50_MOUSE	P06329 mus musculu
22	359	48.1	117	1	HV1G_HUMAN	P23083 homo sapien
23	356.5	47.8	136	1	HV16_MOUSE	P01783 mus musculu
24	321.5	43.1	114	1	HV00_MOUSE	P01741 mus musculu
25	316.5	42.4	119	1	HV38_MOUSE	P01808 mus musculu
26	315	42.2	117	1	HV42_MOUSE	P01812 mus musculu
27	314	42.1	117	1	HV1A_HUMAN	P01742 homo sapien
28	312.5	41.9	119	1	HV37_MOUSE	P01807 mus musculu
29	311	41.7	142	1	HV01_RAT	P01805 rattus norv
30	310.5	41.6	119	1	HV40_MOUSE	P01810 mus musculu
31	304	40.8	118	1	HV39_MOUSE	P01809 mus musculu
32	297	39.8	137	1	HV46_MOUSE	P01822 mus musculu
33	297	39.8	144	1	HV26_MOUSE	P01795 mus musculu
34	293.5	39.3	120	1	HV1H_HUMAN	P80421 homo sapien
35	292	39.1	117	1	HV41_MOUSE	P01811 mus musculu
36	291.5	39.1	116	1	HV05_CARAU	P19181 carassius a
37	290	38.9	116	1	HV36_MOUSE	P01806 mus musculu
38	290	38.9	123	1	HV24_MOUSE	P01793 mus musculu
39	288	38.6	117	1	HV3C_HUMAN	P01764 homo sapien
40	285.5	38.3	116	1	HV3T_HUMAN	P01781 homo sapien
41	284.5	38.1	122	1	HV3G_HUMAN	P01768 homo sapien
42	284	38.1	144	1	HV43_MOUSE	P01819 mus musculu
43	284	38.1	146	1	HV2I_HUMAN	P06331 homo sapien
44	282.5	37.9	122	1	HV3A_HUMAN	P01762 homo sapien
45	282	37.8	125	1	HV1F_HUMAN	P06326 homo sapien

ALIGNMENTS

RESULT 1
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC ---
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CC or send an email to license@isb-sib.ch).
CC ---
DR EMBL; J00529; AAA38170.1; -.
DR PIR; A02034; MHMS18.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 62.3%; Score 464.5; DB 1; Length 139;
Best Local Similarity 65.0%; Pred. No. 8.1e-38;

```
  Matches   91;  Conservative   18;  Mismatches   28;  Indels    3;  Gaps    1;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |  | :| || |  |||:|:||||| ||||||||||||||| |||:     ::| |||||
Db       1 MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           :|||||||||| :| |||: ||: |||:| |  |:|||:|||||||||:|||:|||  |
Db      61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDY 120

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           ||:      |||||||::||
Db     121 YGS---SYFDYWGQGTTLTV 137


RESULT   2
HV02_MOUSE
ID   HV02_MOUSE     STANDARD;      PRT;   140 AA.
AC   P01746;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A/J;
RX   MEDLINE=82152818; PubMed=6801765;
RA   Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA   Capra J.D.;
RT   "Somatic mutation in genes for the variable portion of the
RT   immunoglobulin heavy chain.";
RL   Science 216:309-311(1982).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00493; AAA38128.1; -.
DR   PIR; A02028; HVMSG7.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    140       IG HEAVY CHAIN V REGION 93G7.
FT   NON_TER     140    140
SQ   SEQUENCE   140 AA;  15514 MW;  25A4CBBE31DA5CE8 CRC64;


  Query Match             61.5%;  Score 459;  DB 1;  Length 140;
  Best Local Similarity   63.6%;  Pred. No. 2.7e-37;
  Matches   89;  Conservative   18;  Mismatches   31;  Indels    2;  Gaps    1;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |  |::  ||::|  ||:|||||||||||||: |:|||:|| |||:      |: |||||
Db       1 MGWSFIFLFLLSVTAGVHSEVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||  |:| |||  |: ||:|| |:| | ||:|||:|| ||||||:|||||||  |
Db      61 GQGLEWIGYINPGNGYINYNEKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSHY 120

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           ||  | |  |||||||  :||
Db     121 YG--GSYDFDYWGQGTPLTV 138


RESULT   3
HV03_MOUSE
ID   HV03_MOUSE     STANDARD;      PRT;   120 AA.
AC   P01747;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 36-65.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83131846; PubMed=6186498;
RA   Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA   Marshak-Rothstein A.;
RT   "The genetic basis of antibody production: the dominant anti-arsonate
RT   idiotype response of the strain A mouse.";
RL   Eur. J. Immunol. 12:1023-1032(1982).
CC   -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC       DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC       CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC       SEGMENT, JH2.
DR   PIR; A02028; HVMSG7.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13307 MW;  FF04E4A167B654AF CRC64;


  Query Match             57.0%;  Score 425;  DB 1;  Length 120;
  Best Local Similarity   68.3%;  Pred. No. 4.2e-34;
  Matches   82;  Conservative   14;  Mismatches   22;  Indels    2;  Gaps    1;

Qy      21 VQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYD 80
           ||||||||||: |:|||:|| |||:      |: ||||| ||||||| |:| ||||||:
Db       1 VQLQQSGAELVRAGSSVKMSCKASGYTFTSYGINWVKQRPGQGLEWIGYINPGNGYTKYN 60

Qy      81 PKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
           ||:|| |:| | ||:|||:|| |||||:|||||||  |||  | |  |||||||::||
Db      61 EKFKGKTTLTVDKSSSTAYMQLRSLTSEDSAVYFCARSVYYG--GSYYFDYWGQGTTLTV 118


RESULT   4
HV11_MOUSE
ID   HV11_MOUSE     STANDARD;      PRT;   137 AA.
AC   P01755;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC       MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC       (NPB ANTIBODIES).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; J00539; AAA38172.1; -.
DR   PIR; A02038; G2MS43.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    137       IG HEAVY CHAIN V REGION S43.
FT   DOMAIN       20     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DOMAIN      118    122       D SEGMENT.
FT   DOMAIN      123    137       JH2 SEGMENT.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     137    137
SQ   SEQUENCE   137 AA;  15200 MW;  ADD5881BF44B8EC9 CRC64;


  Query Match             56.6%;  Score 422.5;  DB 1;  Length 137;
  Best Local Similarity   61.4%;  Pred. No. 8.4e-34;
  Matches   86;  Conservative   16;  Mismatches   33;  Indels    5;  Gaps    2;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |  | :| || |  |||:|:||||| ||| |||||||||| |||:      :| | |||
Db       1 MGWSCIMLFLAATATGVHSQVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
             :|||||||||| :| | |:  |: |||:| |  |:|||:||||||||:|||:|||
Db      61 GRGLEWIGRIDPNSGGTTYNEHFRSKATLTIDKPSSTAYMQLSSLTSEDSAVYYCARY-R 119

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
             | |     |||||||::||
Db     120 LGRY----FDYWGQGTTLTV 135


RESULT   5
HV48_MOUSE
ID   HV48_MOUSE     STANDARD;      PRT;   138 AA.
AC   P03980;
DT   23-OCT-1986 (Rel. 02, Created)
DT   23-OCT-1986 (Rel. 02, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84248078; PubMed=6429663;
RA   Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA   Tucker P.W.;
RT   "Illegitimate recombination generates a class switch from C mu to C
RT   delta in an IgD-secreting plasmacytoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR   PIR; A02033; HVMST7.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    138       IG HEAVY CHAIN V REGION TEPC 1017.
FT   DOMAIN       21     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DOMAIN      118    127       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      128    138       FRAMEWORK 4.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     138    138
SQ   SEQUENCE   138 AA;  15576 MW;  748157E4C6907B8E CRC64;


  Query Match             55.8%;  Score 416;  DB 1;  Length 138;
  Best Local Similarity   60.0%;  Pred. No. 3.6e-33;
  Matches   84;  Conservative   21;  Mismatches   29;  Indels    6;  Gaps    2;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |  |::: ||:|   | |:|:||||| |||||||||||:||| |||    : :|| |||||
Db       1 MGWSYIILFLVATATDVHSQVQLQQPGAELVKPGASVQLSCKASGHTFTNYWIHWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-EG 119
             ||||||| |:| :| : |: ||: |||:| | ||:|||:|||||| |: |||:||| :|
Db      61 GQGLEWIGEINPNDGRSNYNEKFKNKATLTVDKSSSTAYMQLSSLTPEEFAVYYCARSDG 120

Qy     120 YYGNYGVYAMDYWGQGTSVT 139
             ||  :      |||||| ||
Db     121 YYDWF-----VYWGQGTLVT 135


RESULT   6
HV09_MOUSE
ID   HV09_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01753; P11271;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 186-1 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR   PIR; B02034; HVMS61.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION 186-1.
FT   DOMAIN       20     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12890 MW;  16191A088CB17F5A CRC64;


  Query Match             55.1%;  Score 411;  DB 1;  Length 117;
  Best Local Similarity   68.4%;  Pred. No. 8.9e-33;
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  Matches   80;  Conservative   15;  Mismatches   22;  Indels    0;  Gaps    0;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |  | :| || |  |||:|:||||| |||||||||||||| |||:     ::| |||||
Db       1 MGWSCIMLFLAATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
           :|||||||||| :| |||: ||: |||:| ||||:|||:|| ||||||:|||:|||
Db      61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDTSSSTAYMQLHSLTSEDSAVYYCAR 117


RESULT   7
HV15_MOUSE
ID   HV15_MOUSE     STANDARD;      PRT;   136 AA.
AC   P01759;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION BCL1 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82222262; PubMed=6806821;
RA   Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA   Blattner F.R.;
RT   "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT   by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT   by two adjacent CH genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00494; AAA38130.1; -.
DR   PIR; A02042; HVMSB1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    136       IG HEAVY CHAIN V REGION BCL1.
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  15078 MW;  6827CFBC6DB3F35E CRC64;


  Query Match             53.1%;  Score 396;  DB 1;  Length 136;
  Best Local Similarity   55.7%;  Pred. No. 2.9e-31;
  Matches   78;  Conservative   23;  Mismatches   33;  Indels    6;  Gaps    2;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |  | ::|||:|  |||:|:|||||| |:|:|| |||:||  ||:   |  :| |||
Db       1 MGWSCIIFFLVATATGVHSQVQLQQSGPEVVRPGVSVKISCKGSGYTFTDYAMHWVKQSH 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
            : ||||| |   || | |: ||:||||:| | ||:| :::|: |||||:|  :|||  |
Db      61 AKSLEWIGVISTYNGNTSYNQKFKGKATMTVDKSSSTVHMELARLTSEDSANLYCAR--Y 118

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           ||||     |||||||::||
Db     119 YGNY----FDYWGQGTTLTV 134


RESULT   8
HV06_MOUSE
ID   HV06_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01750;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 102 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR   PIR; A02032; HVMS02.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       IG HEAVY CHAIN V REGION 102.
FT   DOMAIN       20     49       FRAMEWORK 1.
FT   DOMAIN       50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       55     68       FRAMEWORK 2.
FT   DOMAIN       69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       86    117       FRAMEWORK 3.
FT   DISULFID     41    115       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12867 MW;  740A65DD851FCA8C CRC64;


  Query Match             52.7%;  Score 393;  DB 1;  Length 117;
  Best Local Similarity   65.5%;  Pred. No. 4.8e-31;
  Matches   76;  Conservative   17;  Mismatches   23;  Indels    0;  Gaps    0;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |  | :: ||:|  |||:| |||||  |||||||||||||:|| |||:     ::| |||||
Db       1 MGWSCIILFLVATATGVHSHVQLQQPGAELVKPGASVKVSCKASGYTFTSYWMHWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCA 116
            |||||||| |::  | |: ||:||||:| | ||:|||:||||||||:|||:||
Db      61 GQGLEWIGRIHPSDSDTNYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116


RESULT   9
HV49_MOUSE
ID   HV49_MOUSE     STANDARD;      PRT;   117 AA.
AC   P06328;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION VH558 B4 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85099340; PubMed=2578321;
RA   Yancopoulos G.D., Alt F.W.;
RT   "Developmentally controlled and tissue-specific expression of
RT   unrearranged VH gene segments.";
RL   Cell 40:271-281(1985).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M13788; AAA38506.1; -.
DR   PIR; A02035; MHMSB4.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    117       IG HEAVY CHAIN V REGION VH558 B4.
FT   DOMAIN      20     49       FRAMEWORK 1.
FT   DOMAIN      50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      55     68       FRAMEWORK 2.
FT   DOMAIN      69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      86    117       FRAMEWORK 3.
FT   DISULFID    41    115       BY SIMILARITY.
FT   NON_TER    117    117
SQ   SEQUENCE   117 AA;  12834 MW;  B8862FAC67ABD345 CRC64;

  Query Match             52.7%;  Score 393;  DB 1;  Length 117;
  Best Local Similarity   65.8%;  Pred. No. 4.8e-31;
  Matches   77;  Conservative   14;  Mismatches   26;  Indels    0;  Gaps    0;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |  | :| || |  |||:| ||||| |||||||||||||||| |||:     ::| |||||
Db       1 MGWSCIMLFLAATATGVHSPVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
             :|||||| ||| :| |||: ||: |||:| |  |:|||:|||||||||:|||:| |
Db      61 GRGLEWIGNIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCTR 117


RESULT  10
HV10_MOUSE
ID   HV10_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01754; P11270;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 145 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J00533; AAA38602.1; -.
DR   PIR; C02034; HVMS45.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    117       IG HEAVY CHAIN V REGION 145.
FT   DOMAIN      20     49       FRAMEWORK 1.
FT   DOMAIN      50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      55     68       FRAMEWORK 2.
FT   DOMAIN      69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      86    117       FRAMEWORK 3.
FT   NON_TER    117    117
SQ   SEQUENCE   117 AA;  12921 MW;  D37DE8A3F543E996 CRC64;

  Query Match             52.1%;  Score 389;  DB 1;  Length 117;
  Best Local Similarity   65.8%;  Pred. No. 1.1e-30;
  Matches   77;  Conservative   15;  Mismatches   25;  Indels    0;  Gaps    0;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |  | :| || |  |||: :||||| ||||||||||||||  |||:     ::| |||||
Db       1 MGWSCIMLFLAATATGVHFQVQLQQPGAELVKPGASVKLSSKASGYTFTSYWMHWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
             :|||||||||| :| |||: ||: |||:| |  |:|||:|||||||||:|||:|||
Db      61 GRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR 117


RESULT  11
HV04_MOUSE
ID   HV04_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01748;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION 23 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=81234548; PubMed=6788376;
RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
CC   -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC       RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR   PIR; A02030; HVMS23.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    117       IG HEAVY CHAIN V REGION 23.
FT   DOMAIN      20     49       FRAMEWORK 1.
FT   DOMAIN      50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      55     68       FRAMEWORK 2.
FT   DOMAIN      69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      86    117       FRAMEWORK 3.
FT   DISULFID    41    115       BY SIMILARITY.
FT   NON_TER    117    117
SQ   SEQUENCE   117 AA;  12772 MW;  C530F829C906F69B CRC64;

  Query Match             52.0%;  Score 388;  DB 1;  Length 117;
  Best Local Similarity   64.1%;  Pred. No. 1.4e-30;
  Matches   75;  Conservative   15;  Mismatches   27;  Indels    0;  Gaps    0;
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Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |  | :: ||:|   ||:|:||||| | |||||||||||| |||:     ::| |||||
Db       1 MGWSCIILFLVAAANGVHSQVQLQQPGTELVKPGASVKLSCKASGYTFTSYWMHWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
           ||||||| |:| || | |: ||: | |:| | ||:||| |||||||||:|||:|||
Db      61 GQGLEWIGNINPGNGGTNYNEKFKSKVTLTVDKSSSTAYTQLSSLTSEDSAVYYCAR 117


RESULT 12
HV52_MOUSE
ID   HV52_MOUSE      STANDARD;      PRT;   117 AA.
AC   P06327;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION VH558 A1/A4 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85099340; PubMed=2578321;
RA   Yancopoulos G.D., Alt F.W.;
RT   "Developmentally controlled and tissue-specific expression of
RT   unrearranged VH gene segments.";
RL   Cell 40:271-281(1985).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M13787; AAA38499.1; -.
DR   PIR; A02029; HVMSA1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    117       IG HEAVY CHAIN V REGION VH558 A1/A4.
FT   DOMAIN      20     49       FRAMEWORK 1.
FT   DOMAIN      50     54       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      55     68       FRAMEWORK 2.
FT   DOMAIN      69     85       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      86    117       FRAMEWORK 3.
FT   DISULFID    41    115       BY SIMILARITY.
FT   NON_TER    117    117
SQ   SEQUENCE   117 AA;  12971 MW;  8B0BC138856DFC9D CRC64;


  Query Match             51.1%;  Score 381;  DB 1;  Length 117;
  Best Local Similarity   65.5%;  Pred. No. 6.7e-30;
  Matches   74;  Conservative   16;  Mismatches   23;  Indels    0;  Gaps    0;

Qy       5 WVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGL 64
           |:  ||::   ||: :||||||| ||||||| ||:|| |||:       |: ||||| |||
Db       5 WIFLFLLSGTAGVHCQVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPGQGL 64

Qy      65 EWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
           |||| | | :| ||| ||:|||||:||| ||:|||:|||||||||::|||||||
Db      65 EWIGWIYPGDGSTKYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR 117


RESULT 13
HV13_MOUSE
ID   HV13_MOUSE      STANDARD;      PRT;   117 AA.
AC   P01757;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION J558.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=80078170; PubMed=6765983;
RA   Schilling J., Clevinger B., Davie J.M., Hood L.;
RT   "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT   rearrangements in heavy chain V-region gene segments.";
RL   Nature 283:35-40(1980).
CC   -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC       BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC       WHICH OCCUR IN THE D AND J SEGMENTS.
CC   -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR   PIR; A26242; MHMSJ5.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DISULFID     22     96       BY SIMILARITY.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13024 MW;  292E2AF4BE447E41 CRC64;


  Query Match             50.8%;  Score 379;  DB 1;  Length 117;
  Best Local Similarity   62.0%;  Pred. No. 1e-29;
  Matches   75;  Conservative   16;  Mismatches   24;  Indels    6;  Gaps    1;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           |||||||| ||||||||||:|| |||:   | |:  |||   : ||||| |:| || | |
Db       1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
           : ||:||||:| | ||:|||:||:||||||:|||:|||: |      :  | || ||:||
Db      61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY------WYFDVWGAGTTVT 114

Qy     140 V 140
           |
Db     115 V 115


RESULT 14
HV01_MOUSE
ID   HV01_MOUSE      STANDARD;      PRT;   121 AA.
AC   P01745;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG HEAVY CHAIN V REGION MPC 11.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81053741; PubMed=6253904;
RA   Zakut R., Cohen J., Givol D.;
RT   "Cloning and sequence of the cDNA corresponding to the variable
RT   region of immunoglobulin heavy chain MPC11.";
RL   Nucleic Acids Res. 8:3591-3601(1980).
RN   [2]
RP   REVISIONS.
RA   Zakut R., Cohen J., Givol D.;
RL   Nucleic Acids Res. 8:4839-4840(1980).
CC   -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC       FROM A MYELOMA THAT SECRETES IGG2B.
```

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DR   PIR; A02027; GVMS11.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13135 MW;  227AEF3EC56ED0BF CRC64;


  Query Match             50.8%;  Score 379;  DB 1;  Length 121;
  Best Local Similarity   62.0%;  Pred. No. 1.1e-29;
  Matches   75;  Conservative   17;  Mismatches   27;  Indels    2;  Gaps    2;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           | ||||||||||:|| |||:|| |:|:   : :|  ||:||  |||||| | |  |:| |
Db       1 EAQLQQSGAELVRPGTSVKISCKAAGYTFTNYWIGWVKERPGHGLEWIGDIYPGGGFTNY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
           :   :||||:||||||:|||:||||||||||:|:| ||| | | |   |  | |||||::|
Db      61 NDNLKGKATLTADTSSSTAYIQLSSLTSEDSAIYHCAR-GIYYNSSPY-FDSWGQGTTLT 118

Qy     140 V 140
           |
Db     119 V 119


RESULT  15
HV1C_HUMAN
ID   HV1C_HUMAN     STANDARD;      PRT;   147 AA.
AC   P01744;
DT   21-JUL-1986 (Rel. 01, Created)
DT   20-AUG-2001 (Rel. 40, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   IG HEAVY CHAIN V-I REGION ND PRECURSOR (FRAGMENTS).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83065234; PubMed=6815656;
RA   Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA   Bell L.O., Gould H.J.;
RT   "Cloning and sequence determination of the gene for the human
RT   immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL   Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN   [2]
RP   SEQUENCE OF 20-147.
RA   Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL   (In) Bach M.K. (eds.);
RL   Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL   Marcel Dekker, New York (1978).
CC   -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA
CC       PROTEIN.
DR   PIR; A02026; E1HUND.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    147       IG HEAVY CHAIN V-I REGION ND.
FT   MOD_RES      20     20       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     41    115
FT   CONFLICT     21     21       T -> V (IN REF. 2).
FT   CONFLICT     53     54       IH -> HI (IN REF. 2).
FT   CONFLICT     67     68       VG -> GV (IN REF. 2).
FT   CONFLICT    125    125       MISSING (IN REF. 2).
FT   NON_TER     147    147
SQ   SEQUENCE   147 AA;  16491 MW;  948F9F72A5366C20 CRC64;


  Query Match             50.7%;  Score 378.5;  DB 1;  Length 147;
  Best Local Similarity   52.6%;  Pred. No. 1.5e-29;
  Matches   72;  Conservative   25;  Mismatches   35;  Indels    5;  Gaps    1;

Qy       9 FLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIG 68
           ||:|  | |:|: || |||||: ||||||::|| |||:   |:||| ::| |  ||||:|
Db       9 FLVAAATRVHSQTQLVQSGAEVRKPGASVRVSCKASGYTFIDSYIHWIRQAPGHGLEWVG 68

Qy      69 RIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR-----EGYYGN 123
             |:| :| | | |:|||: |:| | | :|||: | || |:|:||::||:       ||
Db      69 WINPNSGGTNYAPRFQGRVTMTRDASFSTAYMDLRSLRSDDSAVFYCAKSDPFWSDYYNF 128

Qy     124 YGVYAMDYWGQGTSVTV 140
             | :| |||||:|||
Db     129 DYSYTLDVWGQGTTVTV 145


Search completed: May  7, 2002, 12:32:34
Job time: 565 sec
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:22:25 ; Search time 67.39 Seconds
(without alignments)
116.512 Million cell updates/sec

Title: US-09-155-739-7
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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9: /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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11: /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
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17: /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT:*
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19: /SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	562	100.0	106	16	AAR81321	Humanized anti-VLA
2	562	100.0	106	18	AAW22412	Humanised alpha-4
3	562	100.0	126	18	AAW22419	Humanised alpha-4
4	508	90.4	106	16	AAR81328	Mouse anti-VLA-4 a
5	508	90.4	126	16	AAR81326	Mouse VLA-4 antibo
6	508	90.4	126	16	AAR81332	Human VLA-4 reshap
7	508	90.4	126	18	AAW22409	Alpha-4 integrin m
8	488	86.8	359	20	AAY29913	Human MCP-3 and mu
9	488	86.8	361	20	AAY29911	Human IP-10 and mu
10	488	86.8	374	20	AAY29916	Artificial synthet
11	481	85.6	128	15	AAR60627	ME1-14 light chain
12	475.5	84.6	234	12	AAR13050	CD4-specific CDR-g
13	471.5	83.9	107	16	AAR78970	Light chain variab
14	465	82.7	108	17	AAR93159	Murine monoclonal
15	460.5	81.9	128	11	AAR06252	Variable region of
16	460	81.9	637	13	AAR26983	(FRP51)-ETA fusion
17	456	81.1	109	19	AAW26797	Anti-gp54 MAb T16
18	455	81.0	240	16	AAR85495	ScFv(FWP51). Synt
19	455	81.0	241	20	AAY21882	Amino acid sequenc
20	455	81.0	245	19	AAW26800	Anti-gp54 MAb T16
21	453.5	80.7	107	16	AAR81322	Humanized VLA-4 an
22	453.5	80.7	107	18	AAW22422	Humanised alpha-4
23	453	80.6	109	12	AAR13658	Murine OKT4A light
24	452	80.4	241	13	AAR26981	FWP51 fusion prote
25	451.5	80.3	108	16	AAR65163	Human REI monoclon
26	451.5	80.3	129	15	AAR47207	Human/murine IL-1
27	451	80.2	355	18	AAW35133	R. pipiens recombi
28	449.5	80.0	107	19	AAW86805	Variable Light dom
29	449.5	80.0	107	19	AAW70625	Humanised murine a
30	446.5	79.4	108	18	AAW10231	CDR-grafted light
31	446.5	79.4	110	19	AAW70673	Anti-VEGF humanise
32	446.5	79.4	234	18	AAW10233	TF8-5G9 CDR-grafte
33	446.5	79.4	237	19	AAW70703	Protein encoded by
34	445.5	79.3	107	19	AAW86804	Variable Light dom
35	445.5	79.3	107	19	AAW70623	Humanised murine a
36	444.5	79.1	107	20	AAW87455	Humanised anti-alp
37	444.5	79.1	107	22	AAB62087	Human Vl consensus
38	444.5	79.1	107	22	AAB60400	Consensus human li
39	444.5	79.1	107	22	AAB61585	Human variable lig
40	444.5	79.1	108	19	AAW70622	Human consensus fr
41	444.5	79.1	108	21	AAY82345	Human consensus se
42	444.5	79.1	126	13	AAR29015	pUC-RVl-PM1a. Syn
43	444.5	79.1	126	13	AAR29013	pUC-RVh-PM1a. Syn
44	444.5	79.1	256	21	AAY55072	Interleukin-6 spec
45	444.5	79.1	260	21	AAY55075	Single chain Fv pr

ALIGNMENTS

RESULT 1
AAR81321
ID AAR81321 standard; Protein; 106 AA.
XX
AC AAR81321;
XX
DT 02-APR-1996 (first entry)
XX
DE Humanized anti-VLA-4 antibody 21.6 light chain variable region, La.
XX
KW Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW antibody engineering.
XX
OS Chimeric Mus musculus.
OS Chimeric Homo sapiens.
XX
PN WO9519790-A1.
XX
PD 27-JUL-1995.
XX
PF 25-JAN-1995; 95WO-US01219.
XX
PR 25-JAN-1994; 94US-0186269.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones TS, Leger OJ, Saldanha J;
XX
DR WPI; 1995-269276/35.
XX
PT New humanised antibodies against VLA-4 - used for inhibiting
PT leukocyte adhesion to endothelial cells, partic. for treating
PT inflammatory disease.
XX

```
PS   Claim 9; Page 67; 105pp; English.
XX
CC   The sequence encodes the humanized mouse antibody 21.6 light chain
CC   variable region, La, directed against leukocyte adhesion molecule
CC   VLA-4. Cloned cDNA sequences of mouse 21.6 VL and VH (AAQ99889 and
CC   AAQ99892) regions are linked to human constant regions in the
CC   construction of a humanized antibody against VLA-4. The 5' and 3'
CC   ends of the mouse cDNAs are modified using PCR primers (See
CC   AAQ99895-98) and then subcloned into mammalian cell expression vectors
CC   containing human kappa or gamma-1 constant regions. In the humanized
CC   light chain, amino acids L45, L49, L58 and L69 in the human kappa LC
CC   VR framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig L chain. Plasmids encoding the chimeric
CC   antibodies are transfected into COS cells. The humanized antibodies
CC   can be used for inhibiting adhesion of a leukocyte to an endothelial
CC   cell and for treating inflammatory diseases such as multiple
CC   sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can
CC   also be used for detecting VLA-4, for affinity purification or for
CC   generating anti-idiotype antibodies.
XX
SQ   Sequence   106 AA;


  Query Match             100.0%;  Score 562;  DB 16;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-37;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Db       1 diqmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||||||||||||||||||||||||||||||||||||||
Db      61 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 106


RESULT   2
AAW22412
ID   AAW22412 standard; Protein; 106 AA.
XX
AC   AAW22412;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL La.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1..23
FT                   /label= FR1
FT                   /note= "REI framework region 1"
FT   Region          24..34
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          35..49
FT                   /label= FR2
FT                   /note= "REI framework region 2"
FT   Misc-difference 45
FT                   /note= "REI Lys-45 is substd. by Lys of mouse
FT                          21.6 VL, important in supporting the
FT                          CDR2 loop"
FT   Misc-difference 49
FT                   /note= "REI Tyr-49 is substd. by His of mouse
FT                          21.6 VL, located at the binding site"
FT   Region          50..56
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          57..88
FT                   /label= FR3
FT                   /note= "REI framework region 3"
FT   Misc-difference 58
FT                   /note= "REI Val-58 is substd. by Ile of mouse
FT                          21.6 VL, important in supporting the CDR2
FT                          loop"
FT   Misc-difference 69
FT                   /note= "REI Thr-69 is substd. by Arg of mouse
FT                          21.6 VL, involved in antibody-antigen
FT                          binding"
FT   Region          89..96
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Region          97..106
FT                   /label= FR4
FT                   /note= "REI framework region 4"
FT   Misc-difference 103
FT                   /note= "REI Leu-103 substd. by Val, more typical
FT                          of human kappa light chain J region"
FT   Misc-difference 104
FT                   /note= "REI Gln-104 substd. by Glu, more typical
FT                          of human kappa light chain J region"
FT   Misc-difference 106
FT                   /note= "REI Thr-106 substd. by Lys, more typical
FT                          of human kappa light chain J region"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones ST,  Leger OJ,  Saldanha J,  Yednock TA;
XX
DR   WPI; 1997-297879/27.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Claim 25; Fig 6; 107pp; English.
XX
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6.  It is
CC   composed of complementarity determining regions (CDRs) from the VL
CC   region (see AAW22409) of mouse alpha-4 integrin monoclonal antibody
CC   21.6 and a modified human REI framework.  It can be expressed in
CC   mammalian host cells following PCR amplification and mutagenesis
CC   of appropriate fragments of mouse and human DNA sequences.  The
CC   humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury.  The antibody
CC   may also be used in the affinity purification of alpha-4 integrin
CC   for use as a vaccine or an immunogen.  It is also useful for
CC   generating idiotypic antibodies.  The humanised antibody has a
CC   half-life in the human circulation essentially equivalent to that
CC   of naturally occurring human antibodies.
XX
SQ   Sequence   106 AA;
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  Query Match             100.0%;  Score 562;  DB 18;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-37;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 diqmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||||||||||||||||||||||||||||||||||||||||||
Db      61 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 106


RESULT   3
AAW22419
ID   AAW22419 standard; Protein; 126 AA.
XX
AC   AAW22419;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Humanised alpha-4 integrin antibody 21.6 VL version La.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Chimeric Mus musculus;
OS   Chimeric Homo sapiens;
OS   Chimeric synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Leader
FT   Protein         21..126
FT                   /label= Mat_protein
FT                   /note= "VL version La (Claim 25)"
FT   Region          21..43
FT                   /label= FR1
FT                   /note= "REI framework region 1"
FT   Region          44..54
FT                   /label= CDR1
FT                   /note= "21.6 complementarity determining region 1"
FT   Region          55..69
FT                   /label= FR2
FT                   /note= "REI framework region 2"
FT   Region          70..76
FT                   /label= CDR2
FT                   /note= "21.6 complementarity determining region 2"
FT   Region          77..108
FT                   /label= FR3
FT                   /note= "REI framework region 3"
FT   Region          109..116
FT                   /label= CDR3
FT                   /note= "21.6 complementarity determining region 3"
FT   Region          117..126
FT                   /label= FR4
FT                   /note= "REI framework region 4"
XX
PN   WO9718838-A1.
XX
PD   29-MAY-1997.
XX
PF   21-NOV-1996;   96WO-US18807.
XX
PR   21-NOV-1995;   95US-0561521.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones ST,  Leger OJ,  Saldanha J,  Yednock TA;
XX
DR   WPI; 1997-297879/27.
DR   N-PSDB; AAT74788.
XX
PT   Uses of humanised alpha-4 integrin antibody - for treatment of
PT   asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS   Example 6; Fig 10; 107pp; English.
XX
CC   This polypeptide, designated La, comprises the light chain variable
CC   region (VL) of a humanised alpha-4 integrin antibody 21.6 (see also
CC   AAW22412).  It is composed of complementarity determining regions from
CC   the VL region (see AAW22409) of mouse alpha-4 integrin monoclonal
CC   antibody 21.6 and a modified human REI framework.  It can be
CC   expressed in mammalian host cells following PCR amplification and
CC   mutagenesis of appropriate mouse and human DNA sequences.  The
CC   humanised 21.6 VL and a humanised 21.6 VH (see AAW22413) can be used
CC   to produce a claimed humanised 21.6 antibody that is useful in the
CC   manufacture of a medicament for treating asthma, atherosclerosis,
CC   AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
CC   arthritis, transplant rejection, graft versus host disease, tumour
CC   metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC   ischaemia, and acute leukocyte mediated lung injury.  The humanised
CC   antibody has a half-life in the human circulation essentially
CC   equivalent to that of naturally occurring human antibodies.
XX
SQ   Sequence   126 AA;


  Query Match             100.0%;  Score 562;  DB 18;  Length 126;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-37;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21 diqmtqspsslsasvgdrvtitcktsqdinkymawyqqtpgkaprllihytsalqpgips 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||||||||||||||||||||||||||||||||||||||
Db      81 rfsgsgsgrdytftisslqpediatyyclqydnlwtfgqgtkveik 126


RESULT   4
AAR81328
ID   AAR81328 standard; Protein; 106 AA.
XX
AC   AAR81328;
XX
DT   02-APR-1996  (first entry)
XX
DE   Mouse anti-VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Region          1..23
FT                   /label= FR1
FT                   /note= "mouse light chain variable framework
FT                         region 1"
FT   Region          24..34
FT                   /label= CDR1
FT                   /note= "mouse light chain variable complementarity
FT                         determining region 1"
FT   Region          35..49
FT                   /label= FR2
FT                   /note= "mouse light chain variable framework
FT                         region 2"
FT   Region          50..56
FT                   /label= CDR2
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FT                      /note= "mouse light chain variable complementarity
FT                       determining region 2"
FT   Region             57..88
FT                      /label= FR3
FT                      /note= "mouse light chain variable framework
FT                       region 3"
FT   Region             89..96
FT                      /label= CDR3
FT                      /note= "mouse light chain variable complementarity
FT                       determining region 3"
FT   Region             97..106
FT                      /label= FR4
FT                      /note= "mouse light chain variable framework
FT                       region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Page 66; 105pp; English.
XX
CC   The sequence represents the mouse anti-VLA-4 antibody 21.6 light chain
CC   variable region (without signal sequence). Cloned cDNA CDR sequences of
CC   mouse 21.6 variable light and variable heavy regions are linked to human
CC   constant framework regions of the REI antibody for the light chain and
CC   the 2*CL antibody for the heavy chain in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions. In the humanized light chain, amino acids L45, L49,
CC   L58 and L69 in the human kappa LCVR framework are replaced by the amino
CC   acid present in the equivalent position of the mouse 21.6 Ig light
CC   chain. Plasmids encoding the chimeric antibodies are transfected into COS
CC   cells. The humanized antibodies can be used to inhibit adhesion of a
CC   leukocyte to an endothelial cell and to treat inflammatory diseases such
CC   as multiple sclerosis. They can also be used in the treatment of stroke,
CC   cerebral traumas, meningitis or encephalitis. The antibodies can also be
CC   used for detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   106 AA;


  Query Match             90.4%;  Score 508;  DB 16;  Length 106;
  Best Local Similarity   88.7%;  Pred. No. 1.1e-32;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

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           |||||||||||||:| :||||||||||||||||||  ||| ||||||||||||||||
Db       1 diqmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||||||:| ||:|:|||||||||||||||||| |||:|||
Db      61 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 106


RESULT   5
AAR81326
ID   AAR81326 standard; Protein; 126 AA.
XX
AC   AAR81326;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Mouse VLA-4 antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /note= "signal peptide"
FT   Region          21..43
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /note= "framework region 3"
FT   Region          109..116
FT                   /note= "complementarity determining region 3"
FT   Region          117..126
FT                   /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99889.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 1; 105pp; English.
XX
CC   The sequence represents the mouse antibody 21.6 light chain variable
CC   region directed against leukocyte adhesion molecule VLA-4.  Cloned
CC   cDNA sequences of mouse 21.6 VL and VH (see AAQ99892) regions are
CC   linked to human constant regions in the construction of a humanized
CC   antibody against VLA-4.  The 5' and 3' ends of the mouse cDNAs are
CC   modified using PCR primers (See AAQ99895-98) and then subcloned into
CC   mammalian cell expression vectors containing human kappa or gamma-1
CC   constant regions.  In the humanized light chain, amino acids L45,
CC   L49, L58 and L69 in the human kappa LC VR framework are replaced
CC   by the amino acid present in the equivalent position of the mouse
CC   21.6 Ig L chain.  Plasmids encoding the chimeric antibodies are
CC   transfected into COS cells.  The humanized antibodies can be used
CC   to inhibit adhesion of a leukocyte to an endothelial cell and
CC   to treat inflammatory diseases such as multiple sclerosis.  They
CC   can also be used in the treatment of stroke, cerebral traumas,
CC   meningitis or encephalitis.  The antibodies can also be used for
CC   detecting VLA-4, for affinity purification or for generating
CC   anti-idiotype antibodies.
XX
SQ   Sequence   126 AA;
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  Query Match             90.4%;  Score 508;  DB 16;  Length 126;
  Best Local Similarity   88.7%;  Pred. No. 1.2e-32;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :||||||||||||||||||  ||| ||||||||||||||||
Db      21 diqmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||||||:| ||:|:||||||||||||||||||| |||:|||
Db      81 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 126


RESULT   6
AAR81332
ID   AAR81332 standard; Protein; 126 AA.
XX
AC   AAR81332;
XX
DT   23-MAR-1996  (first entry)
XX
DE   Human VLA-4 reshaped antibody 21.6 light chain variable region.
XX
KW   Humanized antibody; leukocyte adhesion molecule; VLA-4; therapeutic;
KW   antibody engineering.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /note= "signal peptide"
FT   Region          21..43
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /note= "framework region 3"
FT   Region          109..116
FT                   /note= "complementarity determining region 3"
FT   Region          117..126
FT                   /note= "framework region 4"
XX
PN   WO9519790-A1.
XX
PD   27-JUL-1995.
XX
PF   25-JAN-1995;   95WO-US01219.
XX
PR   25-JAN-1994;   94US-0186269.
XX
PA   (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI   Bendig MM,  Jones TS,  Leger OJ,  Saldanha J;
XX
DR   WPI; 1995-269276/35.
DR   N-PSDB; AAQ99893.
XX
PT   New humanised antibodies against VLA-4 - used for inhibiting
PT   leukocyte adhesion to endothelial cells, partic. for treating
PT   inflammatory disease.
XX
PS   Disclosure; Fig 10; 105pp; English.
XX
CC   The sequence represents the human reshaped antibody 21.6 light
CC   chain variable region against leukocyte adhesion molecule VLA-4.
CC   Cloned cDNA sequences of mouse 21.6 VL (AAQ99889) and VH (AAQ99892)
CC   regions are linked to human constant regions in the construction
CC   of a humanized antibody against VLA-4.  The 5' and 3' ends of the
CC   mouse cDNAs are modified using PCR primers (See AAQ99895-98) and
CC   then subcloned into mammalian cell expression vectors containing
CC   human kappa or gamma-1 constant regions.  In the humanized light
CC   chain, amino acids L45, L49, L58 and L69 in the human kappa LC VR
CC   framework are replaced by the amino acid present in the equivalent
CC   position of the mouse 21.6 Ig L chain.  Plasmids encoding the
CC   chimeric antibodies are transfected into COS cells.  The humanized
CC   antibodies can be used to inhibit adhesion of a leukocyte to an
CC   endothelial cell and to treat inflammatory diseases such as
CC   multiple sclerosis.  They can also be used in the treatment of
CC   stroke, cerebral traumas, meningitis or encephalitis.  The
CC   antibodies can also be used for detecting VLA-4, for affinity
CC   purification or for generating anti-idiotype antibodies.
XX
SQ   Sequence   126 AA;


  Query Match             90.4%;  Score 508;  DB 16;  Length 126;
  Best Local Similarity   88.7%;  Pred. No. 1.2e-32;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :||||||||||||||||||  ||| ||||||||||||||||
Db      21 diqmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||||||:| ||:|:||||||||||||||||||| |||:|||
Db      81 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 126


RESULT   7
AAW22409
ID   AAW22409 standard; Protein; 126 AA.
XX
AC   AAW22409;
XX
DT   08-DEC-1997  (first entry)
XX
DE   Alpha-4 integrin mouse MAb 21.6 VL region.
XX
KW   Alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
KW   asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
KW   metastasis; inflammatory bowel disease; rheumatoid arthritis;
KW   transplant rejection; graft versus host disease; nephritis;
KW   atopic dermatitis; psoriasis; myocardial ischaemia;
KW   acute leukocyte mediated lung injury; therapy.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Leader
FT   Region          21..43
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          44..54
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1"
FT   Region          55..69
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          70..76
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2"
FT   Region          77..108
FT                   /label= FR3
FT                   /note= "framework region 3"
FT   Region          109..116
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3"
FT   Region          117..126
FT                   /label= FR4
FT                   /note= "framework region 4"
XX
```

PN WO9718838-A1.
XX
PD 29-MAY-1997.
XX
PF 21-NOV-1996; 96WO-US18807.
XX
PR 21-NOV-1995; 95US-0561521.
XX
PA (ATHE-) ATHENA NEUROSCIENCES INC.
XX
PI Bendig MM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
XX
DR WPI; 1997-297879/27.
DR N-PSDB; AAT74759.
XX
PT Uses of humanised alpha-4 integrin antibody - for treatment of
PT asthma, atherosclerosis, AIDS, dementia, etc.
XX
PS Claim 18; Page 68; 107pp; English.
XX
CC This polypeptide comprises the light chain variable region (VL) of
CC mouse anti-alpha-4 integrin monoclonal antibody 21.6. The
CC complementarity determining regions (CDRs) of the 21.6 VL can be
CC incorporated into a human REI framework to produce a claimed
CC humanised 21.6 VL (see AAW22412) and a claimed humanised 21.6
CC antibody that is used in the manufacture of a medicament for
CC treating a disease selected from asthma, atherosclerosis, AIDS,
CC dementia, diabetes, inflammatory bowel disease, rheumatoid
CC arthritis, transplant rejection, graft versus host disease, tumour
CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
CC ischaemia, and acute leukocyte mediated lung injury. The antibody
CC may also be used in the affinity purification of alpha-4 integrin
CC for use as a vaccine or an immunogen. It is also useful for
CC generating idiotypic antibodies. The humanised antibodies of the
CC invention have a half-life in the human circulation essentially
CC equivalent to that of naturally occurring human antibodies.
XX
SQ Sequence 126 AA;

Query Match 90.4%; Score 508; DB 18; Length 126;
Best Local Similarity 88.7%; Pred. No. 1.2e-32;
Matches 94; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

```
Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||:| :|||||||||||||||||||  ||| ||||||||||||||||
Db      21 diqmtqspsslsaslggkvtitcktsqdinkymawyqhkpgkrprllihytsalqpgips 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||||:| ||:|:|||||||||||||||||||| |||:|||
Db      81 rfsgsgsgrdysfnisnlepediatyyclqydnlwtfgggtkleik 126
```

RESULT 8
AAY29913
ID AAY29913 standard; Protein; 359 AA.
XX
AC AAY29913;
XX
DT 17-NOV-1999 (first entry)
XX
DE Human MCP-3 and murine scFv38 fusion protein.
XX
KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW immune response; HIV; infection.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
PN WO9946392-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05345.
XX
PR 12-MAR-1998; 98US-0077745.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kwak LW, Biragyn A;
XX
DR WPI; 1999-551418/46.
XX
PT New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection -
XX
PS Disclosure; Page 118-119; 142pp; English.
XX
CC The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC be used for producing an immune response, e.g. an effector T cell immune
CC response. They can also be used for treating cancer or treating or
CC preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC can be used in in vitro diagnostic assays, as well as in screening assays
CC for identifying unknown tumour antigen epitopes and fine mapping of
CC tumour antigen epitopes. The present sequence represents a fusion protein
CC from the present invention.
XX
SQ Sequence 359 AA;

Query Match 86.8%; Score 488; DB 20; Length 359;
Best Local Similarity 84.9%; Pred. No. 1.1e-30;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

```
Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||:| :|||||| |||||||:||||  ||| |||||||||| |||||||
Db     233 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 292

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:|:||:|:|||||||||||||||:||| |||:|||
Db     293 rfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 338
```

RESULT 9
AAY29911
ID AAY29911 standard; Protein; 361 AA.
XX
AC AAY29911;
XX
DT 17-NOV-1999 (first entry)
XX
DE Human IP-10 and murine scFv38 fusion protein.
XX
KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW immune response; HIV; infection.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
XX
PN WO9946392-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05345.
XX
PR 12-MAR-1998; 98US-0077745.

XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kwak LW, Biragyn A;
XX
DR WPI; 1999-551418/46.
XX
PT New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection -
XX
PS Disclosure; Page 115-116; 142pp; English.
XX
CC The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion proteins
CC comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and human
CC Muc-1; (2) human interferon-induced protein 10 (IP-10) and human Muc-1;
CC (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4) human
CC SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human MCP-3 and
CC HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and HIV
CC gp120. The fusion proteins, and nucleotide sequences encoding them, can
CC be used for producing an immune response, e.g. an effector T cell immune
CC response. They can also be used for treating cancer or treating or
CC preventing HIV infection. The fusion proteins and/or nucleotide sequences
CC can be used in in vitro diagnostic assays, as well as in screening assays
CC for identifying unknown tumour antigen epitopes and fine mapping of
CC tumour antigen epitopes. The present sequence represents a fusion protein
CC from the present invention.
XX
SQ Sequence 361 AA;

Query Match 86.8%; Score 488; DB 20; Length 361;
Best Local Similarity 84.9%; Pred. No. 1.1e-30;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

```
Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||||||||||:| :|||||| |||||||:||||  ||| |||||||||| |||||||
Db     235 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 294

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
          ||||||||||:|:||:|:|||||||||||||:||| |||:|||
Db     295 rfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 340
```

RESULT 10
AAY29916
ID AAY29916 standard; Protein; 374 AA.
XX
AC AAY29916;
XX
DT 17-NOV-1999 (first entry)
XX
DE Artificial synthetic construct protein SEQ ID NO:15.
XX
KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW immune response; HIV; infection.
XX
OS Synthetic.
XX
PN WO9946392-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05345.
XX
PR 12-MAR-1998; 98US-0077745.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kwak LW, Biragyn A;
XX
DR WPI; 1999-551418/46.
XX
PT New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection -
XX
PS Disclosure; Page 117-118; 142pp; English.
XX
CC The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion
CC proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and
CC human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human
CC Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)
CC human SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human
CC MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and
CC HIV gp120. The fusion proteins, and nucleotide sequences encoding them,
CC can be used for producing an immune response, e.g. an effector T cell
CC immune response. They can also be used for treating cancer or treating
CC or preventing HIV infection. The fusion proteins and/or nucleotide
CC sequences can be used in in vitro diagnostic assays, as well as in
CC screening assays for identifying unknown tumour antigen epitopes and fine
CC mapping of tumour antigen epitopes. AAY29916 and AAZ21156 to AAZ21168 are
CC sequences given in the SEQ ID LISTING in the present invention but which
CC are not mentioned further within the specification.
XX
SQ Sequence 374 AA;

Query Match 86.8%; Score 488; DB 20; Length 374;
Best Local Similarity 84.9%; Pred. No. 1.2e-30;
Matches 90; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

```
Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          ||||||||||||||:| :|||||| |||||||:||||  ||| |||||||||| |||||||
Db      95 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 154

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
          ||||||||||:|:||:|:|||||||||||||:||| |||:|||
Db     155 rfsgsgsgrdysfsisnlepediatyyclqydnlytfgggtkleik 200
```

RESULT 11
AAR60627
ID AAR60627 standard; Protein; 128 AA.
XX
AC AAR60627;
XX
DT 04-JUN-1995 (first entry)
XX
DE ME1-14 light chain variable region.
XX
KW Monoclonal antibody; tumour.
XX
OS Homo sapiens.
XX
PN WO9421294-A.
XX
PD 29-SEP-1994.
XX
PF 14-MAR-1994; 94WO-US02724.
XX
PR 19-MAR-1993; 93US-0033864.
XX
PA (BIGN/) BIGNER D D.
PA (CARR/) CARREL S.
PA (ZALU/) ZALUTSKY M R.
XX
PI Bigner DD, Carrel S, Zalutsky MR;
XX
DR WPI; 1994-316669/39.
DR N-PSDB; AAQ73537.
XX
PT Method of treating solid or cystic tumours with antibodies - by
PT administering monoclonal antibody Mel-14, having Fc deleted,

```
PT   using injection or deposition in the cyst cavity
XX
PS   Disclosure; Fig 2; 31pp; English.
XX
CC   The sequence is that of the ME1-14 light chain.  The protein is  a
CC   monoclonal antibody which can be administered to treat solid or
CC   cystic tumours.
CC   See also AAR60626.
XX
SQ   Sequence   128 AA;


  Query Match             85.6%;  Score 481;  DB 15;  Length 128;
  Best Local Similarity   84.0%;  Pred. No. 1.6e-30;
  Matches   89;  Conservative    9;  Mismatches    8;  Indels    0;  Gaps    0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||||||||||||||:| :|||||| |||||||:|||| ||| ||||:|||| |||||||
Db     21 diqmtqspssslsaslggkvtitckasqdinkyiawyqhkpgkgprllmhytstlqpgips 80

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
          ||||||||||:|:||:|:|||||||||||||| ||| |||:|||
Db     81 rfsgsgsgrdysfsisnlepediatyyclqydnlltfgggtkleik 126


RESULT  12
AAR13050
ID   AAR13050 standard; Protein; 234 AA.
XX
AC   AAR13050;
XX
DT   27-SEP-1991  (first entry)
XX
DE   CD4-specific CDR-grafted light chain.
XX
KW   variable region; antibody; OKT4A; heavy chain; CD4;
KW   complementarity determining region.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= signal sequence
FT   Region          21..45
FT                   /label= framework region 1
FT   Region          46..52
FT                   /label= CDR 1
FT   Region          53..69
FT                   /label= framework region 2
FT   Region          70..76
FT                   /label= CDR 2
FT   Region          77..110
FT                   /label= framework region 3
FT   Region          111..116
FT                   /label= CDR 3
FT   Region          117..132
FT                   /label= framework region 4
FT   Region          133..234
FT                   /label= kappa constant domain
XX
PN   WO9109966-A.
XX
PD   11-JUL-1991.
XX
PF   21-DEC-1990;   90WO-GB02015.
XX
PR   21-DEC-1989;   89GB-0028874.
PR   21-DEC-1990;   90WO-GB02017.
PR   21-DEC-1990;   90WO-GB02018.
XX
PA   (ORTH ) ORTHO PHARM CORP.
XX
PI   Jolliffe LK,  Zivin RA,  Pulito VL,  Adair JR,  Athwal DS;
XX
DR   WPI; 1991-222914/30.
DR   N-PSDB; AAQ12633.
XX
PT   New CD4 specific recombinant - complementarity determining region
PT   grafted antibody for treating graft rejection and T cell
PT   disorders
XX
PS   Claim 1; Fig 8; 96pp; English.
XX
CC   This is an example of a CDR-grafted light chain of the invention.
CC   The constant regions are based on sequences of the human kappa
CC   constant domain, the signal sequence is derived from murine MAb
CC   B72.3 and the CDR sequences are based on the murine OKT4A light chain
CC   CDRs. The recombinant antibody encoded by this sequence has affinity
CC   for CD4 similar to that of OKT4A.
CC   See also AAQ12627-Q12632.
XX
SQ   Sequence   234 AA;


  Query Match             84.6%;  Score 475.5;  DB 12;  Length 234;
  Best Local Similarity   84.9%;  Pred. No. 7.2e-30;
  Matches   90;  Conservative    8;  Mismatches    7;  Indels    1;  Gaps    1;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||||||||||||||||||||||| | ||| |: |||||||||:|||:||| ||||:||
Db     21 diqmtqspsslsasvgdrvtitckaspdinnylnwyqqtpgkapklliyytstlqpgvps 80

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEI 105
          |||||||| :|||||||||||||||||| |||| |:||||||::|
Db     81 rfsgsgsgteytftisslqpediatyycqqydnllftfgqgtklqi 126


RESULT  13
AAR78970
ID   AAR78970 standard; Protein; 107 AA.
XX
AC   AAR78970;
XX
DT   21-DEC-1995  (first entry)
XX
DE   Light chain variable region for monoclonal antibody 23F8.
XX
KW   Monoclonal antibody; heavy metal; mercury; variable region;
KW   light chain.
XX
OS   Synthetic.
XX
PN   WO9520607-A.
XX
PD   03-AUG-1995.
XX
PF   27-JAN-1995;   95WO-US01199.
XX
PR   27-JAN-1994;   94US-0187407.
XX
PA   (BION-) BIONEBRASKA INC.
XX
PI   Lopez O,  Wagner FW,  Wylie DE;
XX
DR   WPI; 1995-275415/36.
DR   N-PSDB; AAQ97508.
XX
PT   New polypeptide(s) which bind heavy metals, esp. mercury - derived from
PT   monoclonal antibodies, used for detecting, removing, adding or
PT   neutralising heavy metals
XX
PS   Claim 23; Page 67-68; 106pp; English.
XX
CC   Hybridoma antibodies have been produced with the spleen cells of
CC   BALB/c mouse that had received multiple injections of mercuric ions
CC   reacted with glutathione to produce a mercuric ion coordinate
```

```
CC   covalent compound which was covalently bound to keyhole limpet
CC   hemocyanin (KLH). Eight hybridomas (1F10, 4A10, 1C11, 5G4, 23F8, 2D5,
CC   5B6 and 3E8) were producing MAbs that were strongly positive
CC   against glutatione-mercuric ions but negative against glutathione
CC   without mercuric ions. RNA was isolated from hybridoma cells with
CC   guanidine isothiocyanate. First strand cDNA synthesis was catalysed
CC   by MuLv reverse transcriptase. The primers used for cDNA synthesis
CC   were complementary to the 5' end of the CH1 domain of the heavy
CC   chain expressed by the hybridoma of interest, or to the 5' and of
CC   the C kappa domain. Some of the primers used for cDNA synthesis are
CC   shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the
CC   variable region of a particular antibody polypeptide was also used
CC   for PCR amplification of that variable region, in conjunction with
CC   an appropriate V-region primer. In addition, the VH primer AAQ97518
CC   was used to amplify the mAb 2D5 and 5B6 heavy chains. The sequences
CC   of the PCR amplified nucleotides were determined. These are given
CC   in AAQ97498-Q97510 and the deduced AA sequences in AAR79241-R79250 &
CC   AAR78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC   and in the claims are different from the descriptions in the
CC   sequence listings. The descriptions in the sequence listings are
CC   used here.
XX
SQ   Sequence   107 AA;


  Query Match             83.9%;  Score 471.5;  DB 16;  Length 107;
  Best Local Similarity   83.2%;  Pred. No. 7.2e-30;
  Matches   89;  Conservative    9;  Mismatches    8;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :|||||| |||||||:||||  ||| |||||||||| |||||||
Db       1 diqmtqspsslsaslggkvtitckasqdinkyiawyqhkpgkgprllihytstlqpgips 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
           |||||||||||:|:||: :|||||||||||||| |:||| |||:|||
Db      61 rfsgsgsgrdysfsisnpepediatyyclqydnslftfgsgtkleik 107


RESULT  14
AAR93159
ID   AAR93159 standard; Protein; 108 AA.
XX
AC   AAR93159;
XX
DT   24-OCT-1996  (first entry)
XX
DE   Murine monoclonal antibody K20 kappa chain variable region.
XX
KW   Antibody; light chain; kappa; variable region; K20; integrin; CD29;
KW   beta 1 subunit; humanisation; Hu-K20; immunosuppressant;
KW   T cell activation; complementarity determining region; CDR.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Region          1..23
FT                   /label= FR1
FT                   /note= "framework region"
FT   Region          24..34
FT                   /label= CDR1
FT                   /note= "complementarity determining region"
FT   Region          35..49
FT                   /label= FR2
FT                   /note= "framework region"
FT   Region          50..56
FT                   /label= CDR2
FT                   /note= "complementarity determining region"
FT   Region          57..88
FT                   /label= FR3
FT                   /note= "framework region"
FT   Region          89..94
FT                   /label= CDR3
FT                   /note= "complementarity determining region"
FT   Region          95..108
FT                   /label= J_kappa1
XX
PN   FR2724393-A1.
XX
PD   15-MAR-1996.
XX
PF   12-SEP-1994;   94FR-0010858.
XX
PR   12-SEP-1994;   94FR-0010858.
XX
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (PROT-) PROTEINE PERFORMANCE SA.
XX
PI   Bernard A,  Cervoni MF,  Lefranc MP,  Margaritte C;
PI   Poul MA;
XX
DR   WPI; 1996-162083/17.
DR   N-PSDB; AAT26849.
XX
PT   Humanisation of non-human immunoglobulin variable regions - for
PT   prodn. of humanised antibodies, esp. K20, e.g. as an
PT   immunosuppressant
XX
PS   Example 1; Fig 2A; 39pp; French.
XX
CC   The present sequence is that of the variable region of the kappa
CC   light chain from murine monoclonal antibody K20. The antibody
CC   recognises the beta 1 subunit (CD29) of integrins and inhibits
CC   activation and proliferation of peripheral T cells induced by
CC   anti-CD3 antibodies. Monoclonal antibody K20 is a preferred target
CC   for humanisation; the humanised version may be useful as an
CC   immunosuppressant. In the humanisation process, the complementarity
CC   determining regions (CDRs) of a human antibody with framework
CC   regions 70-95% homologous to those of K20 were replaced by the K20
CC   CDRs.
XX
SQ   Sequence   108 AA;


  Query Match             82.7%;  Score 465;  DB 17;  Length 108;
  Best Local Similarity   81.1%;  Pred. No. 2.3e-29;
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Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Db       1 diqltqspsslsasiggkvtitckasqdinkyiawyqhepgkgprllirytsklesgips 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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Db      61 rfsgsgsgrdysfsisnlepediatyyclqyynlwtfgggtkleik 106


RESULT  15
AAR06252
ID   AAR06252 standard; protein; 128 AA.
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AC   AAR06252;
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DT   10-DEC-1990  (first entry)
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DE   Variable region of murine AHT 107 light chain.
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KW   Interleukin-2 receptor; IL-2; tumour necrosis factor; TNF; ss;
XX
OS   Mus sp.
XX
PN   EP380068-A.
XX
PD   01-AUG-1990.
XX
PF   24-JAN-1990;   90EP-0101351.
XX
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PR 04-DEC-1989; 89US-0441702.
PR 24-JAN-1989; 89US-0301216.
XX
PA (MOLE-) MOLECULAR THERAPEU.
XX
PI Zerler B;
XX
DR WPI; 1990-232892/31.
DR N-PSDB; AAQ05556.
XX
PT Expression vectors for producing chimeric monoclonal antibodies -
PT which express human constant region and non-human variable region
XX
PS Disclosure; ; p; English.
XX
CC MAbs comprising mouse CH and CL constant regions whith human
CC variable regions may be used to create mouse/human hybrid MAbs,
CC which have a longer serum half-life. Method can be used to produce
CC Abs against interleukin-2 receptor and tumour necrosis factor.
XX
SQ Sequence 128 AA;

Query Match 81.9%; Score 460.5; DB 11; Length 128;
Best Local Similarity 76.6%; Pred. No. 6e-29;
Matches 82; Conservative 18; Mismatches 6; Indels 1; Gaps 1;

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Db      21 diqmtqspsslsaslggkvtltcktsqdinkfiawyqhkpgegprliihytstlqpgips 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           ||||||||:||:|:|::|:||||||||||:||:| |||| |||:|::
Db      81 rfsgsgsgkdysfsinnlepediatyyclryddlpwtfgggtklevr 127
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Search completed: May 7, 2002, 12:22:25
Job time: 246 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 12:23:04 ; Search time 32.41 Seconds
(without alignments)
73.599 Million cell updates/sec

Title: US-09-155-739-7
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	562	100.0	106	2	US-08-561-521-7	Sequence 7, Appli
2	562	100.0	106	5	PCT-US95-01219-7	Sequence 7, Appl
3	508	90.4	106	2	US-08-561-521-5	Sequence 5, Appli
4	508	90.4	106	5	PCT-US95-01219-5	Sequence 5, Appl
5	508	90.4	126	2	US-08-561-521-2	Sequence 2, Appli
6	508	90.4	126	2	US-08-561-521-15	Sequence 15, Appl
7	508	90.4	126	5	PCT-US95-01219-2	Sequence 2, Appl
8	508	90.4	126	5	PCT-US95-01219-15	Sequence 15, Appl
9	481	85.6	128	1	US-08-339-582-4	Sequence 4, Appli
10	471.5	83.9	107	2	US-08-888-366-22	Sequence 22, Appl
11	460	81.9	637	1	US-08-235-838-16	Sequence 16, Appl
12	460	81.9	637	2	US-08-465-473B-16	Sequence 16, Appl
13	455	81.0	241	1	US-08-235-838-11	Sequence 11, Appl
14	455	81.0	241	2	US-08-465-473B-11	Sequence 11, Appl
15	454.5	80.9	108	2	US-08-602-725-29	Sequence 29, Appl
16	453.5	80.7	107	2	US-08-561-521-8	Sequence 8, Appli
17	453.5	80.7	107	5	PCT-US95-01219-8	Sequence 8, Appli
18	451	80.2	355	3	US-08-875-811-57	Sequence 57, Appl
19	448.5	79.8	107	2	US-07-934-373C-17	Sequence 17, Appl
20	448.5	79.8	107	3	US-08-437-642B-17	Sequence 17, Appl
21	448.5	79.8	107	5	PCT-US93-07832-17	Sequence 17, Appl
22	444.5	79.1	107	2	US-07-934-373C-18	Sequence 18, Appl
23	444.5	79.1	107	3	US-08-437-642B-18	Sequence 18, Appl
24	444.5	79.1	107	5	PCT-US93-07832-18	Sequence 18, Appl
25	444.5	79.1	108	3	US-08-974-899-3	Sequence 3, Appli
26	444.5	79.1	111	1	US-08-137-117D-67	Sequence 67, Appl
27	444.5	79.1	111	2	US-08-436-717-67	Sequence 67, Appl
28	444.5	79.1	126	1	US-08-137-117D-71	Sequence 71, Appl
29	444.5	79.1	126	2	US-08-436-717-71	Sequence 71, Appl
30	443.5	78.9	107	2	US-08-561-521-6	Sequence 6, Appli
31	443.5	78.9	107	2	US-08-652-558-34	Sequence 34, Appl
32	443.5	78.9	107	5	PCT-US95-01219-6	Sequence 6, Appl
33	443.5	78.9	108	2	US-08-070-116A-7	Sequence 7, Appli
34	443.5	78.9	108	2	US-08-116-247-9	Sequence 9, Appli
35	441.5	78.6	107	2	US-08-318-157B-6	Sequence 6, Appli
36	440.5	78.4	107	2	US-08-652-558-2	Sequence 2, Appli
37	440.5	78.4	109	2	US-07-934-373C-3	Sequence 3, Appli
38	440.5	78.4	109	3	US-08-437-642B-3	Sequence 3, Appli
39	440.5	78.4	109	5	PCT-US93-07832-3	Sequence 3, Appl
40	440.5	78.4	214	2	US-07-934-373C-39	Sequence 39, Appl
41	440.5	78.4	214	3	US-08-437-642B-39	Sequence 39, Appl
42	440.5	78.4	214	5	PCT-US93-07832-39	Sequence 39, Appl
43	438.5	78.0	107	4	US-09-254-189-1	Sequence 1, Appli
44	438.5	78.0	109	2	US-07-934-373C-47	Sequence 47, Appl
45	438.5	78.0	109	3	US-08-437-642B-47	Sequence 47, Appl

ALIGNMENTS

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RESULT 1
US-08-561-521-7
; Sequence 7, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  106 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-7

  Query Match            100.0%;  Score 562;  DB 2;  Length 106;
  Best Local Similarity  100.0%;  Pred. No. 1e-45;
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  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||||||||||||||||||||||||||||||||||||||
Db      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106


RESULT   2
PCT-US95-01219-7
; Sequence 7, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  106 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-7


  Query Match             100.0%;  Score 562;  DB 5;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1e-45;
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Db       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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Db      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106


RESULT   3
US-08-561-521-5
; Sequence 5, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  106 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-5


  Query Match             90.4%;  Score 508;  DB 2;  Length 106;
  Best Local Similarity   88.7%;  Pred. No. 1.1e-40;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

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Db       1 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:| ||:|:|||||||||||||||||| |||:|||
Db      61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106


RESULT   4
PCT-US95-01219-5
; Sequence 5, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
```

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;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94105
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/01219
;       FILING DATE:  25-JAN-1995
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/186,269
;       FILING DATE:  25-JAN-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William L.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  15270-14
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-543-9600
;       TELEFAX:  415-543-5043
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  106 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
PCT-US95-01219-5
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  Query Match             90.4%;  Score 508;  DB 5;  Length 106;
  Best Local Similarity   88.7%;  Pred. No. 1.1e-40;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Db       1 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
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Db      61 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 106
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RESULT   5
US-08-561-521-2
; Sequence 2, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-2
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  Query Match             90.4%;  Score 508;  DB 2;  Length 126;
  Best Local Similarity   88.7%;  Pred. No. 1.3e-40;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
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Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:| ||:|:|||||||||||||||||||| |||:|||
Db      81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126
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RESULT   6
US-08-561-521-15
; Sequence 15, Application US/08561521
; Patent No. 5840299
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/561,521
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,269A
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-561-521-15


  Query Match             90.4%;  Score 508;  DB 2;  Length 126;
  Best Local Similarity   88.7%;  Pred. No. 1.3e-40;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||||||||||||||:| :||||||||||||||||||  ||| ||||||||||||||||
Db     21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
          |||||||||||:| ||:|:||||||||||||||||||| |||:|||
Db     81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126


RESULT   7
PCT-US95-01219-2
; Sequence 2, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-2


  Query Match             90.4%;  Score 508;  DB 5;  Length 126;
  Best Local Similarity   88.7%;  Pred. No. 1.3e-40;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||||||||||||||:| :||||||||||||||||||  ||| ||||||||||||||||
Db     21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
          |||||||||||:| ||:|:||||||||||||||||||| |||:|||
Db     81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126


RESULT   8
PCT-US95-01219-15
; Sequence 15, Application PC/TUS9501219
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Leger, Olivier J.
;    APPLICANT:  Saldanha, Jose
;    APPLICANT:  Jones, S. Tarran
;    TITLE OF INVENTION:  Humanized Antibodies Against Leukocyte
;    TITLE OF INVENTION:  Adhesion Molecule VLA-4
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  One Market Plaza, Steuart Tower, Suite 2000
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94105
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01219
;      FILING DATE:  25-JAN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/186,269
;      FILING DATE:  25-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William L.
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15270-14
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-543-9600
;      TELEFAX:  415-543-5043
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01219-15


  Query Match             90.4%;  Score 508;  DB 5;  Length 126;
  Best Local Similarity   88.7%;  Pred. No. 1.3e-40;
  Matches   94;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||||||||||||||:| :||||||||||||||||||  ||| ||||||||||||||||
Db     21 DIQMTQSPSSLSASLGGKVTITCKTSQDINKYMAWYQHKPGKRPRLLIHYTSALQPGIPS 80

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
          |||||||||||:| ||:|:||||||||||||||||||| |||:|||
Db     81 RFSGSGSGRDYSFNISNLEPEDIATYYCLQYDNLWTFGGGTKLEIK 126


RESULT   9
US-08-339-582-4
; Sequence 4, Application US/08339582
; Patent No. 5558852
;  GENERAL INFORMATION:
;    APPLICANT:  Bigner, Darell D.
;    APPLICANT:  Zalutsky, Michael R.
;    APPLICANT:  Carrel, Stefan
```

```
;    TITLE OF INVENTION:  METHOD OF TREATMENT
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kenneth D. Sibley
;      STREET:  P.O. Drawer 34009
;      CITY:  Charlotte
;      STATE:  No. 5558852th Carolina
;      COUNTRY:  USA
;      ZIP:  28234
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/339,582
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/033,864
;      FILING DATE:  19-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Sibley, Kenneth D.
;      REGISTRATION NUMBER:  31,665
;      REFERENCE/DOCKET NUMBER:  5405-89
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  919-420-2200
;      TELEFAX:  919-881-3175
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  128 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-339-582-4


  Query Match             85.6%;  Score 481;  DB 1;  Length 128;
  Best Local Similarity   84.0%;  Pred. No. 4.3e-38;
  Matches   89;  Conservative    9;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           .|||||||||||||:| :|||||| |||||||:|||| ||| ||||:|||| |||||||
Db      21 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLMHYTSTLQPGIPS 80

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||||||:|:||:|:|||||||||||||| ||| |||:|||
Db      81 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLLTFGGGTKLEIK 126


RESULT  10
US-08-888-366-22
; Sequence 22, Application US/08888366
; Patent No. 5972656
;  GENERAL INFORMATION:
;    APPLICANT:  Lopez, Osvaldo
;    APPLICANT:  Wylie, Dwane E.
;    APPLICANT:  Wagner, Fred W.
;    TITLE OF INVENTION:  Mercury Binding Polypeptides and Nucleotides Coding Therefore
;    NUMBER OF SEQUENCES:  39
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  90 South 7th Street, 3100 No. 5972656west Ctr.
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,366
;      FILING DATE:  03-JUL-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/187,407
;      FILING DATE:  27-JAN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,542
;      FILING DATE:  14-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/493,299
;      FILING DATE:  14-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/324,392
;      FILING DATE:  14-MAR-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carter, Charles G.
;      REGISTRATION NUMBER:  35,093
;      REFERENCE/DOCKET NUMBER:  8648.39USC1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-888-366-22


  Query Match             83.9%;  Score 471.5;  DB 2;  Length 107;
  Best Local Similarity   83.2%;  Pred. No. 2.7e-37;
  Matches   89;  Conservative    9;  Mismatches    8;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||:| :|||||| |||||||:|||| ||| ||||:|||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDN-LWTFGQGTKVEIK 106
           |||||||||||:|:||: :|||||||||||||| |:||| |||:|||
Db      61 RFSGSGSGRDYSFSISNPEPEDIATYYCLQYDNSLFTFGSGTKLEIK 107


RESULT  11
US-08-235-838-16
; Sequence 16, Application US/08235838
; Patent No. 5571894
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5571894man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CIBA-GEIGY Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/235,838
;      FILING DATE:  TBA
```

```
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elmer, James Scott
;      REGISTRATION NUMBER:  36,129
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)541-8614
;      TELEFAX:  (919)541-8689
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-235-838-16


  Query Match             81.9%;  Score 460;  DB 1;  Length 637;
  Best Local Similarity   80.2%;  Pred. No. 2.3e-35;
  Matches   85;  Conservative   10;  Mismatches   11;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||:||||||||||:|  |||||| |||| ||:||||  |||:|||||||||| |||||||
Db     168 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 227

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:|:|: :|:||||||||||| || |:||| |||:|||
Db     228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273


RESULT  12
US-08-465-473B-16
; Sequence 16, Application US/08465473B
; Patent No. 5939531
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5939531man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NOVARTIS Corporation
;      STREET:  564 Morris Avenue
;      CITY:  Summit
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07901-6940
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,473B
;      FILING DATE:  5 June 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pfeiffer, Hesna J.
;      REGISTRATION NUMBER:  22,640
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)522 6940
;      TELEFAX:  (908)522 6955
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  637 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-465-473B-16


  Query Match             81.9%;  Score 460;  DB 2;  Length 637;
  Best Local Similarity   80.2%;  Pred. No. 2.3e-35;
  Matches   85;  Conservative   10;  Mismatches   11;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||:||||||||||:|  |||||| |||| ||:||||  |||:|||||||||| |||||||
Db     168 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 227

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:|:|: :|:||||||||||| || |:||| |||:|||
Db     228 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEIK 273


RESULT  13
US-08-235-838-11
; Sequence 11, Application US/08235838
; Patent No. 5571894
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5571894man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CIBA-GEIGY Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/235,838
;      FILING DATE:  TBA
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elmer, James Scott
;      REGISTRATION NUMBER:  36,129
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)541-8614
;      TELEFAX:  (919)541-8689
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  241 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-235-838-11


  Query Match             81.0%;  Score 455;  DB 1;  Length 241;
  Best Local Similarity   80.0%;  Pred. No. 2.3e-35;
  Matches   84;  Conservative   10;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||:||||||||||:|  |||||| |||| ||:|||  |||:|||||||||| |||||||
Db    137 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 196

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI 105
          |||||||||||:|:| :|:|||||||||| || |:||| |||:||
Db    197 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241


RESULT  14
US-08-465-473B-11
; Sequence 11, Application US/08465473B
; Patent No. 5939531
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5939531man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NOVARTIS Corporation
;      STREET:  564 Morris Avenue
;      CITY:  Summit
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07901-6940
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,473B
;      FILING DATE:  5 June 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pfeiffer, Hesna J.
;      REGISTRATION NUMBER:  22,640
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)522 6940
;      TELEFAX:  (908)522 6955
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  241 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-465-473B-11


  Query Match             81.0%;  Score 455;  DB 2;  Length 241;
  Best Local Similarity   80.0%;  Pred. No. 2.3e-35;
  Matches   84;  Conservative   10;  Mismatches   11;  Indels    0;  Gaps    0;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||:||||||||||:|  |||||| |||| ||:|||  |||:|||||||||| |||||||
Db    137 DIQLTQSPSSLSASLGGEVTITCKASQDIKKYIAWYQHKPGKSPRLLIHYTSVLQPGIPS 196

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEI 105
          |||||||||||:|:| :|:|||||||||| || |:||| |||:||
Db    197 RFSGSGSGRDYSFSIHNLEPEDIATYYCLHYDYLYTFGGGTKLEI 241


RESULT  15
US-08-602-725-29
; Sequence 29, Application US/08602725
; Patent No. 5965710
;  GENERAL INFORMATION:
;    APPLICANT:  BODMER, WALTER F
;    APPLICANT:  DURBIN, HELGA
;    APPLICANT:  SNARY, DAVID
;    APPLICANT:  STEWART, LORNA MD
;    APPLICANT:  YOUNG, SUSAN
;    APPLICANT:  BATES, PAUL A
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES FOR USE IN
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD, 8TH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,725
;      FILING DATE:  02-FEB-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB94/01816
;      FILING DATE:  19-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9317423
;      FILING DATE:  21-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36663
;      REFERENCE/DOCKET NUMBER:  1090-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-816-4091
;      TELEFAX:  703-816-4100
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Hukan REI light chain
US-08-602-725-29


  Query Match             80.9%;  Score 454.5;  DB 2;  Length 108;
  Best Local Similarity   83.0%;  Pred. No. 1.1e-35;
  Matches   88;  Conservative    8;  Mismatches    9;  Indels    1;  Gaps    1;
```

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Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: |||| ||:||||||||||||:|||:  | || |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLAWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
           |||||||| |||||||||||||||||| || :| :|||||||:||
Db      61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKIEI 106
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Search completed: May 7, 2002, 12:23:04
Job time: 175 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 7, 2002, 12:31:42 ; Search time 67.26 Seconds
(without alignments)
304.462 Million cell updates/sec

Title: US-09-155-739-4
Perfect score: 746
Sequence: 1 MKCSWVMFFLMAVVTGVNSE.....YGNYGVYAMDYWGQGTSVTV 140

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	589	79.0	468	11	Q99L31	Q99131 mus musculu
2	494.5	66.3	473	11	Q99L25	Q99125 mus musculu
3	480	64.3	109	11	Q9JL85	Q9jl85 mus musculu
4	478	64.1	473	11	Q9D8L4	Q9d8l4 mus musculu
5	425.5	57.0	463	11	Q99LC4	Q99lc4 mus musculu
6	412	55.2	117	11	Q9QXE9	Q9qxe9 mus musculu
7	388.5	52.1	118	11	Q9Z1C4	Q9z1c4 mus musculu
8	387	51.9	117	11	Q9QXF0	Q9qxf0 mus musculu
9	383.5	51.4	110	11	Q9JL77	Q9jl77 mus musculu
10	380	50.9	111	11	Q9D9B8	Q9d9b8 mus musculu
11	376.5	50.5	109	11	Q9JL75	Q9jl75 mus musculu
12	375.5	50.3	114	11	Q9JL81	Q9jl81 mus musculu
13	371.5	49.8	124	4	Q9UL92	Q9ul92 homo sapien
14	369	49.5	484	11	Q99LA6	Q99la6 mus musculu
15	367	49.2	150	4	Q9Y298	Q9y298 homo sapien
16	366.5	49.1	500	4	Q9BRV0	Q9brv0 homo sapien
17	361	48.4	157	4	O95978	O95978 homo sapien
18	353	47.3	119	5	Q9GYZ2	Q9gyz2 schistosoma
19	350	46.9	119	4	Q9UL94	Q9ul94 homo sapien
20	348.5	46.7	110	11	Q9JL83	Q9jl83 mus musculu
21	343	46.0	125	4	Q9UL95	Q9ul95 homo sapien
22	340.5	45.6	487	11	Q99KA4	Q99ka4 mus musculu
23	338	45.3	117	11	Q9Z1C6	Q9z1c6 mus musculu
24	324.5	43.5	116	4	Q9UL89	Q9ul89 homo sapien
25	322.5	43.2	298	11	Q9QYF0	Q9qyf0 mus musculu
26	302.5	40.5	150	4	O95973	O95973 homo sapien
27	301	40.3	120	4	Q9BUA1	Q9bua1 homo sapien
28	295	39.5	597	4	Q9BQB8	Q9bqb8 homo sapien
29	294.5	39.5	118	4	Q9UL72	Q9ul72 homo sapien
30	294	39.4	119	4	Q9UL73	Q9ul73 homo sapien
31	294	39.4	597	4	Q9BU10	Q9bu10 homo sapien
32	291.5	39.1	112	4	Q9HCC1	Q9hcc1 homo sapien
33	290	38.9	113	4	Q9UL90	Q9ul90 homo sapien
34	285	38.2	131	4	Q9UL88	Q9ul88 homo sapien
35	284.5	38.1	121	11	Q99NG4	Q99ng4 mus musculu
36	281.5	37.7	147	4	Q9Y509	Q9y509 homo sapien
37	279	37.4	116	4	Q9UL93	Q9ul93 homo sapien
38	279	37.4	479	11	Q99M22	Q99m22 mus musculu
39	275	36.9	121	4	Q9UL71	Q9ul71 homo sapien
40	271.5	36.4	124	6	Q9N0W6	Q9n0w6 oryctolagus
41	269.5	36.1	124	6	Q9N0W4	Q9n0w4 oryctolagus
42	267.5	35.9	118	4	Q9UL91	Q9ul91 homo sapien
43	265.5	35.6	122	4	Q9UL84	Q9ul84 homo sapien
44	263.5	35.3	437	11	Q9R1A4	Q9r1a4 mus musculu
45	258.5	34.7	426	11	Q9DCD9	Q9dcd9 mus musculu

ALIGNMENTS

RESULT 1
Q99L31
ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060O09 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 79.0%; Score 589; DB 11; Length 468;
Best Local Similarity 81.4%; Pred. No. 2.2e-51;
Matches 114; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

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Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           ||||||:|||||| |||||||||||||||:||||||||||||||||: :| |||||
Db       1 MKCSWVIFFLMAVVIGVNSEVQLQQSGAELVRPGASVKLSCTASGFNIKDSLMHWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||| ||| :| ||| |||| |||||||||||||||||||||||||:|:|||
Db      61 EQGLEWIGWIDPEDGETKYAPKFQDKATITADTSSNTAYLQLSSLTSEDTAIYYCARNLL 120

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           || |     |||||||::||
Db     121 YGGY----YDYWGQGTTITV 136
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RESULT 2
Q99L25
ID Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

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DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SIMILAR TO RIKEN CDNA 1810060O09 GENE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003888; AAH03888.1; -.
SQ   SEQUENCE   473 AA;  52449 MW;  BE9889B7986DA155 CRC64;


  Query Match             66.3%;  Score 494.5;  DB 11;  Length 473;
  Best Local Similarity   67.6%;  Pred. No. 8e-42;
  Matches   96;  Conservative   19;  Mismatches   24;  Indels    3;  Gaps    2;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |: |||  | ::| |||:|:|||||| ||||||||||:||  ||:   |  || |||||
Db       1 MEWSWVFLFFLSVTTGVHSQVQLQQSDAELVKPGASVKISCKVSGYTFTDHTIHWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREG- 119
           |||||||| | | :| ||| |||:|||||:||| ||:|||:||:|||||:|| ||:| |
Db      61 EQGLEWIGYIYPRDGSTKYNEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVCFCSRGGS 120

Qy     120 -YYGNYGVYAMDYWGQGTSVTV 140
            ||| ||:|  |||||||::||
Db     121 IYYG-YGLYYFDYWGQGTTITV 141


RESULT   3
Q9JL85
ID   Q9JL85      PRELIMINARY;      PRT;   109 AA.
AC   Q9JL85;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206021; AAF69319.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     109     109
SQ   SEQUENCE   109 AA;  11944 MW;  DFE615FE6CED4EDE CRC64;


  Query Match             64.3%;  Score 480;  DB 11;  Length 109;
  Best Local Similarity   80.5%;  Pred. No. 3.8e-41;
  Matches   91;  Conservative    8;  Mismatches    8;  Indels    6;  Gaps    1;

Qy      28 AELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKA 87
           |||||||||||||||||||:|||:| |||||||||||||||| |::||||||||||
Db       1 AELVKPGASVKLSCTASGFNIEDTYMHWVKQRPEQGLEWIGRIDPATGHSKYDPKFQGKA 60

Qy      88 TITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
           |||:|||||||||||||||||||||:| |       |    ||||||::||
Db      61 TITSDTSSNTAYLQLSSLTSEDTAVYYCVRR------GAVVFDYWGQGTALTV 107


RESULT   4
Q9D8L4
ID   Q9D8L4      PRELIMINARY;      PRT;   473 AA.
AC   Q9D8L4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   1810060O09RIK PROTEIN.
GN   1810060O09RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AK007918; BAB25349.1; -.
DR   MGD; MGI:1924014; 1810060O09Rik.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 4.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   473 AA;  51699 MW;  9DED57A514475FBB CRC64;


  Query Match             64.1%;  Score 478;  DB 11;  Length 473;
  Best Local Similarity   67.1%;  Pred. No. 3.7e-40;
  Matches   94;  Conservative   19;  Mismatches   23;  Indels    4;  Gaps    2;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |: |||  ||::|  ||: :|||:||||||||||||:|| |||:   | ||: |||||
Db       1 MEWSWVFLFLLSVTAGVHCQVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||||:| | :| | |: ||:||||:||| ||:|||:||||||||:||||||| ||
Db      61 GQGLEWIGKIGPGSGSTYYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCARSGY 120

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
             :|  :|  |||||| |||
Db     121 --DYDWFA--YWGQGTLVTV 136
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RESULT   5
Q99LC4
ID   Q99LC4      PRELIMINARY;      PRT;   463 AA.
AC   Q99LC4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SIMILAR TO RIKEN CDNA 1810060O09 GENE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003435; AAH03435.1; -.
SQ   SEQUENCE   463 AA;  51007 MW;  EAA674C6BBC30783 CRC64;


  Query Match             57.0%;  Score 425.5;  DB 11;  Length 463;
  Best Local Similarity   59.3%;  Pred. No. 7.3e-35;
  Matches   83;  Conservative   21;  Mismatches   33;  Indels    3;  Gaps    2;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |:  |:  |:::   ||:|:|||||||||| :|||||:||| |||:      :  ||||
Db       1 MEWIWIFLFILSGTAGVHSQVQLQQSGAELARPGASVRLSCKASGYTFTGYGVSWVKQRT 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
           |||||:| | | :| | |  ||:||||:| | ||:|||: ||||||||:|||||||  |
Db      61 GQGLEWVGEIYPGSGNTYYSEKFKGKATLTTDKSSSTAYMHLSSLTSEDSAVYFCARSSY 120

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
           | :| ::|  |||||| |||
Db     121 Y-SYDLFA--YWGQGTLVTV 137


RESULT   6
Q9QXE9
ID   Q9QXE9      PRELIMINARY;      PRT;   117 AA.
AC   Q9QXE9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AJ225174; CAB65237.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13000 MW;  CDDE2AF84D499734 CRC64;


  Query Match             55.2%;  Score 412;  DB 11;  Length 117;
  Best Local Similarity   66.9%;  Pred. No. 3.1e-34;
  Matches   81;  Conservative   14;  Mismatches   20;  Indels    6;  Gaps    1;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           |||||||| ||||||||||:|| |||:   | |:  |||   : ||||| |:| || | |

Db       1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVT 139
           : ||:||||:| | ||:|||:||:||||||:|||:|||: |      ||||||||||||
Db      61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRY------YAMDYWGQGTSVT 114

Qy     140 V 140
           |
Db     115 V 115


RESULT   7
Q9Z1C4
ID   Q9Z1C4      PRELIMINARY;      PRT;   118 AA.
AC   Q9Z1C4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA   Matis L.M., Evans M.J.;
RT   "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT   IgG2/G4 constant regions block human leukocyte binding to porcine
RT   endothelial cells.";
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; U78801; AAD00293.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13036 MW;  90EEC559D31EC4FC CRC64;


  Query Match             52.1%;  Score 388.5;  DB 11;  Length 118;
  Best Local Similarity   62.1%;  Pred. No. 7.5e-32;
  Matches   77;  Conservative   16;  Mismatches   20;  Indels   11;  Gaps    2;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           :||:|||||| :| |||||||| |||:|    ::  ||||| ||||||| | | :| | |
Db       1 QVQVQQSGAELARPWASVKLSCKASGYNFNSYWMQWVKQRPGQGLEWIGAIYPGDGDTSY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCARE---GYYGNYGVYAMDYWGQGT 136
           ||:||||:||| ||:|||:||||| |||:|||:|||    ||:        |||||||
Db      61 TQKFRGKATLTADKSSSTAYMQLSSLASEDSAVYYCARRTVGGYF--------DYWGQGT 112

Qy     137 SVTV 140
           ::||
Db     113 TLTV 116


RESULT   8
Q9QXF0
ID   Q9QXF0      PRELIMINARY;      PRT;   117 AA.
AC   Q9QXF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
```

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RN   [1]
RP   SEQUENCE FROM N.A.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AJ225171; CAB65236.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13060 MW;  D816AD0858A47E4C CRC64;


  Query Match             51.9%;  Score 387;  DB 11;  Length 117;
  Best Local Similarity   63.1%;  Pred. No. 1e-31;
  Matches   77;  Conservative   16;  Mismatches   21;  Indels    8;  Gaps    2;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           |||||||| |||||||||||:|| |||:   | |:  |||    : ||||| |:| || | |
Db       1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCARE-GYYGNYGVYAMDYWGQGTSV 138
           : ||:|||||:| | ||:|||:||:|||||||:|||:|||:  ||        |||||||::
Db      61 NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDKDYY-------FDYWGQGTTL 113

Qy     139 TV 140
           ||
Db     114 TV 115


RESULT   9
Q9JL77
ID   Q9JL77      PRELIMINARY;      PRT;   110 AA.
AC   Q9JL77;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DBA/2;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206029; AAF69327.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     110    110
SQ   SEQUENCE   110 AA;  12138 MW;  2EDE81FB5862C9AF CRC64;


  Query Match             51.4%;  Score 383.5;  DB 11;  Length 110;
  Best Local Similarity   65.8%;  Pred. No. 2.2e-31;
  Matches   73;  Conservative   15;  Mismatches   18;  Indels    5;  Gaps    1;

Qy      30 LVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKATI 89
           ||:|||||||||| |||:    :::|  |||| ||||||| | | :|:| |: ||:||||:
Db       3 LVRPGASVKLSCKASGYTFTSSWMHWAKQRPGQGLEWIGEIHPNSGHTNYNEKFKGKATL 62

Qy      90 TADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
           | |||||:|||: |||||||||:|||:|||:        |||||||||||||
Db      63 TVDTSSSTAYVDLSSLTSEDSAVYYCARQRRN-----YAMDYWGQGTSVTV 108


RESULT  10
Q9D9B8
ID   Q9D9B8      PRELIMINARY;      PRT;   111 AA.
AC   Q9D9B8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ADULT MALE TESTIS CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE   CLONE:1700110L11, FULL INSERT SEQUENCE.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=TESTIS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AK007163; BAB24877.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
SQ   SEQUENCE   111 AA;  11976 MW;  874DDF7BD98BD7B2 CRC64;


  Query Match             50.9%;  Score 380;  DB 11;  Length 111;
  Best Local Similarity   70.2%;  Pred. No. 5e-31;
  Matches   73;  Conservative   17;  Mismatches   14;  Indels    0;  Gaps    0;

Qy      14 VTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPA 73
           :|||:|:|||||||| |||||||||:|| |||:    :::: ||||| :||||||||  |
Db       1 MTGVHSQVQLQQSGPELVKPGASVKISCKASGYAFSSSWMNWVKQRPGKGLEWIGRIYPG 60

Qy      74 NGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAR 117
           :| | |: ||:||||:||| ||:|||:|||||||||:|||||||
Db      61 DGDTNYNGKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAR 104


RESULT  11
Q9JL75
ID   Q9JL75      PRELIMINARY;      PRT;   109 AA.
AC   Q9JL75;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
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DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206031; AAF69329.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  12118 MW;  FF65E441BBF936A6 CRC64;


  Query Match             50.5%;  Score 376.5;  DB 11;  Length 109;
  Best Local Similarity   63.4%;  Pred. No. 1.1e-30;
  Matches   71;  Conservative   18;  Mismatches   18;  Indels    5;  Gaps    1;

Qy      29 ELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKAT 88
           |||||||||||:|| |||:      :| |||:| ||||||| |:| |  |||: ||:|||| 
Db       1 ELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTKYNEKFKGKAT 60

Qy      89 ITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
           :|:| ||:|||::|||||||||:|||:|||:| |  :     |||||||::||
Db      61 LTSDKSSSTAYMELSSLTSEDSAVYYCARDGNYRGF-----DYWGQGTTLTV 107


RESULT  12
Q9JL81
ID   Q9JL81      PRELIMINARY;      PRT;   114 AA.
AC   Q9JL81;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206025; AAF69323.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     114    114
SQ   SEQUENCE   114 AA;  12829 MW;  404885FDE6BA56F8 CRC64;


  Query Match             50.3%;  Score 375.5;  DB 11;  Length 114;
  Best Local Similarity   61.6%;  Pred. No. 1.5e-30;
  Matches   69;  Conservative   21;  Mismatches   21;  Indels    1;  Gaps    1;

Qy      29 ELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKYDPKFQGKAT 88
           :||:|||||||:|| |||::    ::| ||||| ||||||| |||::  |: : ||: |||
Db       2 QLVRPGASVKISCKASGYSFTSYWMHWVKQRPGQGLEWIGMIDPSDSETRLNQKFKDKAT 61

Qy      89 ITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAMDYWGQGTSVTV 140
           :| | ||:|||:|||| ||||:|||:||| |||:  :|  |||||||::||
Db      62 LTVDKSSSTAYMQLSSPTSEDSAVYYCARSNYYGS-SLYYFDYWGQGTTLTV 112


RESULT  13
Q9UL92
ID   Q9UL92      PRELIMINARY;      PRT;   124 AA.
AC   Q9UL92;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035022; AAD56258.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     124    124
SQ   SEQUENCE   124 AA;  13580 MW;  1BAAACBD96ACD2A2 CRC64;


  Query Match             49.8%;  Score 371.5;  DB 4;  Length 124;
  Best Local Similarity   56.6%;  Pred. No. 4.1e-30;
  Matches   73;  Conservative   18;  Mismatches   23;  Indels   15;  Gaps    2;

Qy      20 EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGLEWIGRIDPANGYTKY 79
           |||| :|||| |||||||:|| |||:     |:| |:| | |||||:| |:|: | | |
Db       1 EVQLVESGAEVKKPGASVKVSCKASGYTFSSYYMHWVRQAPGQGLEWMGIINPSGGSTSY 60

Qy      80 DPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNYGVYAM--------DY 131
             ||||: |:| |||::| |::|||| |||||||:|||       |:| :         ||
Db      61 AQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR-------GLYVVVPAAFSRFDY 113

Qy     132 WGQGTSVTV 140
           ||||| |||
Db     114 WGQGTLVTV 122


RESULT  14
Q99LA6
ID   Q99LA6      PRELIMINARY;      PRT;   484 AA.
AC   Q99LA6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   UNKNOWN (PROTEIN FOR MGC:6319).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
```

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RC   TISSUE=MAMMARY TUMOR;
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003495; AAH03495.1; -.
SQ   SEQUENCE   484 AA;  52567 MW;  8EAEA4F9BCF582FA CRC64;


  Query Match             49.5%;  Score 369;  DB 11;  Length 484;
  Best Local Similarity   49.3%;  Pred. No. 4e-29;
  Matches   67;  Conservative   28;  Mismatches   39;  Indels    2;  Gaps    1;

Qy       5 WVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRPEQGL 64
           | : ||||    : :::|| ||| || ||| :||:|| |||:   |  :| ||| | :||
Db       5 WTLLFLMAAAQSIQAQIQLVQSGPELKKPGETVKISCKASGYTFTDYSMHWVKQAPGKGL 64

Qy      65 EWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGYYGNY 124
           :|:| ::   | : |   |:|:   : :||::| :||:::| :|||| ||||| |  :|
Db      65 KWMGWVNIETGESVYADDFKGRFAFSLETSASTIHLQINNLKNEDTATYFCARSDY--DY 122

Qy     125 GVYAMDYWGQGTSVTV 140
           :||||||||||||||
Db     123 DIYAMDYWGQGTSVTV 138


RESULT  15
Q9Y298
ID   Q9Y298      PRELIMINARY;      PRT;   150 AA.
AC   Q9Y298;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   IGG VH PROTEIN PRECURSOR (FRAGMENT).
GN   IGG VH.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98322155; PubMed=9657749;
RA   Jacquemin M.G., Vander Elst L.P.L.;
RT   "Mechanism and kinetics of factor VIII inactivation: study with an
RT   IgG4 monoclonal antibody derived from a hemophilia A patient with
RT   inhibitor.";
RL   Blood 92:496-506(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AJ224083; CAA11829.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   NON_TER     150    150
SQ   SEQUENCE   150 AA;  16031 MW;  563D164AB22802D5 CRC64;


  Query Match             49.2%;  Score 367;  DB 4;  Length 150;
  Best Local Similarity   51.4%;  Pred. No. 1.5e-29;
  Matches   72;  Conservative   24;  Mismatches   38;  Indels    6;  Gaps    1;

Qy       1 MKCSWVMFFLMAVVTGVNSEVQLQQSGAELVKPGASVKLSCTASGFNIKDTYIHCVKQRP 60
           |  :| : ||:|  || :::||| |||||: |||||||:||  ||: : :  :| | | |
Db       1 MDWTWRILFLVAAATGTHAQVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVGQAP 60

Qy      61 EQGLEWIGRIDPANGYTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYFCAREGY 120
            :||||:|  || :| : |  :|||  |:|||||:: ||::|||| |:||||||:||
Db      61 GKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTDIAYMELSSLRSDDTAVYYCAVP-- 118

Qy     121 YGNYGVYAMDYWGQGTSVTV 140
                 | | ||||| |||
Db     119 ----DPDAFDIWGQGTMVTV 134
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Search completed: May  7, 2002, 12:31:42
Job time: 628 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:23:47 ; Search time 37.68 Seconds
(without alignments)
214.291 Million cell updates/sec

Title: US-09-155-739-7
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	488	86.8	104	2	S26330	Ig kappa chain V r
2	479	85.2	104	2	S26329	Ig kappa chain V r
3	478	85.1	106	2	C33936	Ig kappa chain V r
4	463.5	82.5	125	2	S09365	Ig kappa chain - m
5	452	80.4	97	2	PH1064	Ig light chain V r
6	446.5	79.4	107	2	PL0270	Ig kappa chain V r
7	443.5	78.9	108	1	K1HURE	Ig kappa chain V-I
8	443.5	78.9	129	2	S52789	Ig kappa chain V r
9	443	78.8	103	2	S26332	Ig light chain V r
10	440.5	78.4	107	2	PL0272	Ig kappa chain V r
11	440	78.3	94	2	E33730	Ig kappa chain V r
12	439.5	78.2	107	2	PL0269	Ig kappa chain V r
13	439.5	78.2	107	2	PL0271	Ig kappa chain V r
14	439.5	78.2	108	1	K1HUAU	Ig kappa chain V-I
15	435.5	77.5	108	2	I39154	Ig kappa chain (BR
16	429.5	76.4	110	2	S44118	Ig kappa chain V-J
17	429.5	76.4	127	2	S40367	Ig kappa chain V-J
18	426	75.8	107	2	S36275	Ig lambda chain V
19	424.5	75.5	125	2	S40333	Ig kappa chain V-J
20	421.5	75.0	108	1	K1HULY	Ig kappa chain V-I
21	419.5	74.6	108	1	K1HUAG	Ig kappa chain V-I
22	419.5	74.6	108	1	K1HURY	Ig kappa chain V-I
23	418.5	74.5	123	2	S40331	Ig kappa chain - h
24	415.5	73.9	109	2	S31998	Ig kappa chain - h
25	414.5	73.8	131	2	S40352	Ig kappa chain V-J
26	414	73.7	124	2	S40336	Ig kappa chain V-J
27	413.5	73.6	108	1	K1HUSW	Ig kappa chain V-I
28	412.5	73.4	108	2	B49047	Ig kappa chain V r
29	412	73.3	106	2	PC2397	anti-tetanus toxin
30	410.5	73.0	108	2	S44122	Ig kappa chain V r
31	410.5	73.0	109	2	S31981	Ig kappa chain - h
32	409.5	72.9	129	1	K1HUWK	Ig kappa chain pre
33	409	72.8	107	1	K1HUAR	Ig kappa chain V-I
34	408.5	72.7	108	1	K1HUWE	Ig kappa chain V-I
35	408.5	72.7	139	2	S40365	Ig kappa chain - h
36	407.5	72.5	141	2	A49134	Ig kappa chain V-I
37	405.5	72.2	117	2	S46371	Ig kappa chain V-J
38	405	72.1	108	2	S30521	Ig kappa chain V r
39	404.5	72.0	132	2	S40334	Ig kappa chain - h
40	403.5	71.8	94	2	PH1063	Ig light chain V r
41	403.5	71.8	107	2	S36264	Ig lambda chain V
42	403.5	71.8	127	2	S11240	Ig kappa chain V r
43	403	71.7	117	2	S43528	Ig kappa chain V r
44	403	71.7	117	2	S42263	Ig kappa chain V r
45	402.5	71.6	108	1	K1HUHU	Ig kappa chain V-I

ALIGNMENTS

RESULT 1
S26330
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26330
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26330
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59185; NID:g52316; PIDN:CAA41895.1; PID:g1334063
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 86.8%; Score 488; DB 2; Length 104;
Best Local Similarity 85.6%; Pred. No. 1.3e-35;
Matches 89; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

```
Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||:| :|||||| |||||||:|||| ||| |||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
           ||||||||||:|:||:|:|||||||||||||||||| |||:|
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLWTFGGGTKLE 104
```

RESULT 2
S26329
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26329
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-104 <STA>
A;Cross-references: EMBL:X59173; NID:g52309; PIDN:CAA41883.1; PID:g1334059
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

```
  Query Match             85.2%;  Score 479;  DB 2;  Length 104;
  Best Local Similarity   84.6%;  Pred. No. 7.8e-35;
  Matches   88;  Conservative    9;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :|||||| |||||||:||||  ||| |||||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVE 104
           ||||||||||:|:||:|:|||||||||||||:||| |||:|
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKLE 104


RESULT   3
C33936
Ig kappa chain V region (VM113) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000
C;Accession: C33936
R;Meek, K.; Johansson, B.; Schulman, J.; Bona, C.; Capra, J.D.
Proc. Natl. Acad. Sci. U.S.A. 86, 4664-4668, 1989
A;Title: Nucleotide changes in sequential variants of influenza virus hemagglutinin gene
A;Reference number: A33936; MUID:89282831
A;Accession: C33936
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <MEE>
A;Cross-references: GB:J04577; NID:g623187; PIDN:AAA60443.1; PID:g623189
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>


  Query Match             85.1%;  Score 478;  DB 2;  Length 106;
  Best Local Similarity   83.0%;  Pred. No. 9.7e-35;
  Matches   88;  Conservative   10;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :|||||| |||||||:||||  ||| |||||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYLAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           ||||||||||:|:||:| ||:||||||||||:|:||| |||:|||
Db      61 RFSGSGSGRDYSFSISNLDPEEIATYYCLQYDSLYTFGGGTKLEIK 106


RESULT   4
S09365
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S09365
R;Feddersen, R.; van Ness, B.
Nucleic Acids Res. 17, 9797-9809, 1989
A;Title: Direct evidence for intrastrand DNA inversion of kappa immunoglobulin gene segm
A;Reference number: S09365; MUID:90098844
A;Accession: S09365
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <FED>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>


  Query Match             82.5%;  Score 463.5;  DB 2;  Length 125;
  Best Local Similarity   83.2%;  Pred. No. 2e-33;
  Matches   89;  Conservative    7;  Mismatches   10;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :|||||| |||||||:||||  ||| |||||||||| |||||||
Db      18 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 77

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW-TFGQGTKVEIK 106
           |||||||| ||:|:||:| ||||||||||||||  ||| |||:|||
Db      78 RFSGSGSGSDYSFSISNLGPEDIATYYCLQYDNLLRTFGGGTKLEIK 124


RESULT   5
PH1064
Ig light chain V region (clone 202.54) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1064
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A;Reference number: PH0971; MUID:92381444
A;Accession: PH1064
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>


  Query Match             80.4%;  Score 452;  DB 2;  Length 97;
  Best Local Similarity   85.6%;  Pred. No. 1.6e-32;
  Matches   83;  Conservative    8;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :|||||| |||||||:||||  ||| |||||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTF 97
           ||||||||||:|:||:|:|||||||||||||||:||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLFTF 97


RESULT   6
PL0270
Ig kappa chain V region (anti-DNA, 6G6VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0270
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0270
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4


  Query Match             79.4%;  Score 446.5;  DB 2;  Length 107;
  Best Local Similarity   79.4%;  Pred. No. 5.1e-32;
  Matches   85;  Conservative   11;  Mismatches   10;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||| |||||:||:|||||:|||||:| |||||   || ||||| ||| |||||||
Db       1 DIQMTQSPCSLSASLGDKVTITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
```

```
          ||||||||||:|:||:|:||||||||||||| : :||| |||:|||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107
```

RESULT 7
K1HURE
Ig kappa chain V-I region (Rei) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A91663; A01873
R;Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A;Title: Die Primaerstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom k
vollstaendige Aminosaeuresequenz des Proteins.
A;Reference number: A91663; MUID:76023758
A;Accession: A91663
A;Molecule type: protein
A;Residues: 1-108 <PAL>
A;Note: the C region of this chain has the Inv (1,2) marker
R;Epp, O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
Biochemistry 14, 4943-4952, 1975
A;Title: The molecular structure of a dimer composed of the variable portions of the Ben
A;Reference number: A90392; MUID:76039968
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status experimental

Query Match 78.9%; Score 443.5; DB 1; Length 108;
Best Local Similarity 81.1%; Pred. No. 9.4e-32;
Matches 86; Conservative 9; Mismatches 10; Indels 1; Gaps 1;

```
Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: |||| ||: ||||||||||:|||:  | || |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
           ||||||||  |||||||||||||||||||| || :| :|||||||::|
Db      61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106
```

RESULT 8
S52789
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret,
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID:g758589
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 78.9%; Score 443.5; DB 2; Length 129;
Best Local Similarity 79.4%; Pred. No. 1.1e-31;
Matches 85; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

```
Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: |||| |: |||| |||||:|||  |:|: |:||
Db      23 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIHAASSLETGVPS 82

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| |::||||||||||:||||| |||||  ||| |||||||
Db      83 RFSGSGSGTDFSFTISSLQPEDLATYYCQQYDNLPLTFGGGTKVEIK 129
```

RESULT 9
S26332
Ig light chain V region - mouse (fragment)
N;Alternate names: Ig kappa chain V region
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
C;Accession: S26332; S26331
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26332
A;Molecule type: mRNA
A;Residues: 1-103 <STA>
A;Cross-references: EMBL:X59187; NID:g52318; PIDN:CAA41897.1; PID:g1334064
A;Note: the sequence of residues 1-8 and the corresponding nucleic acid sequence are
A;Accession: S26331
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-103 <ST2>
A;Cross-references: EMBL:X59191; NID:g52321; PIDN:CAA41901.1; PID:g1334066
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 443; DB 2; Length 103;
Best Local Similarity 77.7%; Pred. No. 9.9e-32;
Matches 80; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

```
Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:| :|| ||| | || :|:|||| ||| |||:: |||:|||||||
Db       1 DIQMTQSPSSLSASLGGKVTFTCKASHDIKRYIAWYQHKPGKGPRLIMDYTSSLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKV 103
           ||||||||||:|:||:|:|||||||||||||||:||| |||:
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLYTFGGGTKL 103
```

RESULT 10
PL0272
Ig kappa chain V region (anti-DNA, 6B8VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0272
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0272
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

```
  Query Match             78.4%;  Score 440.5;  DB 2;  Length 107;
  Best Local Similarity   78.5%;  Pred. No. 1.7e-31;
  Matches   84;  Conservative   11;  Mismatches   11;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||  |||||:||:| |||:|||||:| |||||    || |||||  ||| |||||||
Db       1 DIQMTQSPCSLSASLGDKVIITCRTSQDISKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||||||:|:||:|:|||||||||||||| : :||| |||:|||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107


RESULT  11
E33730
Ig kappa chain V region (9.42) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C;Accession: E33730
R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A;Reference number: A33730; MUID:89367325
A;Accession: E33730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <LAW>
A;Cross-references: GB:M26000; NID:g197119; PIDN:AAA38916.1; PID:g197120
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>


  Query Match             78.3%;  Score 440;  DB 2;  Length 94;
  Best Local Similarity   86.2%;  Pred. No. 1.6e-31;
  Matches   81;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||:| :|||||| |||||||:|||  ||| |||||||||| |||||||
Db       1 DIQMTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL 94
           |||||||||||:|:||:|:||||||||||||||||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNL 94


RESULT  12
PL0269
Ig kappa chain V region (anti-DNA, 3E12VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0269
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0269
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4


  Query Match             78.2%;  Score 439.5;  DB 2;  Length 107;
  Best Local Similarity   78.5%;  Pred. No. 2.1e-31;
  Matches   84;  Conservative   10;  Mismatches   12;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||:||:| | |:||||| | |||||   || |||||  ||| |||||||
Db       1 DIQMTQSPSSLSASLGDKVIIACRTSQDIRKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||||||:|:||:|:|||||||||||||| : :||| |||:|||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107


RESULT  13
PL0271
Ig kappa chain V region (anti-DNA, 2E3VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0271
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A;Reference number: PL0231; MUID:90111618
A;Accession: PL0271
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4


  Query Match             78.2%;  Score 439.5;  DB 2;  Length 107;
  Best Local Similarity   78.5%;  Pred. No. 2.1e-31;
  Matches   84;  Conservative   10;  Mismatches   12;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||  |||||:||:| |||:|||||  | |||||   || |||||  ||| |||||||
Db       1 DIQMTQSPCSLSASLGDKVIITCRTSQDIRKNMAWYQHKAGKGPRLLIWYTSTLQPGIPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||||||:|:||:|:|||||||||||||| : :||| |||:|||
Db      61 RFSGSGSGRDYSFSISNLEPEDIATYYCLQYDKVPYTFGSGTKLEIK 107


RESULT  14
K1HUAU
Ig kappa chain V-I region (Au) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 21-Jan-2000
C;Accession: A91653; A01862; S02573
R;Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ,
A;Reference number: A91653; MUID:72189444
A;Accession: A91653
A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Note: the C region of this chain has the Inv (3) marker
R;Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; S
Biophys. Struct. Mech. 1, 139-146, 1975
A;Title: The structure determination of the variable portion of the Bence-Jones prote
A;Reference number: A90729; MUID:77022433
A;Contents: annotation; X-ray crystallography
A;Note: the structure of the V region was determined by molecular replacement methods
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances
```

A;Reference number: S02572; MUID:88005152
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 78.2%; Score 439.5; DB 1; Length 108;
Best Local Similarity 79.4%; Pred. No. 2.1e-31;
Matches 85; Conservative 8; Mismatches 13; Indels 1; Gaps 1;

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Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||||||||||||||||||||||: |||| |: |||| ||||| |||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||| |||  :|||||||||||||||| ||| | ||||||||||||
Db      61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK 107
```

RESULT 15
I39154
Ig kappa chain (BRE) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 21-Jan-2000
C;Accession: I39154
R;Schormann, N.; Murrell, J.R.; Liepnieks, J.J.; Benson, M.D.
Proc. Natl. Acad. Sci. U.S.A. 92, 9490-9494, 1995
A;Title: Tertiary structure of an amyloid immunoglobulin light chain protein: A proposed
A;Reference number: I39154; MUID:96003804
A;Accession: I39154
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-108 <RES>
A;Cross-references: EMBL:U31344; NID:g944925; PIDN:AAA79238.1; PID:g944926
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 435.5; DB 2; Length 108;
Best Local Similarity 79.4%; Pred. No. 4.6e-31;
Matches 85; Conservative 9; Mismatches 12; Indels 1; Gaps 1;

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Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: |||| |: |||| |||| |||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLIWYQQKLGKAPNLLIYDASTLETGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| :|||||||||||||||||| |||:| :||||||||||||
Db      61 RFSGSGSGTEYTFTISSLQPEDIATYYCQQYDDLPYTFGQGTKVEIK 107
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Search completed: May 7, 2002, 12:23:47
Job time: 198 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:32:34 ; Search time 21.92 Seconds
(without alignments)
177.303 Million cell updates/sec

Title: US-09-155-739-7
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	443.5	78.9	108	1	KV1O_HUMAN	P01607 homo sapien
2	439.5	78.2	108	1	KV1B_HUMAN	P01594 homo sapien
3	421.5	75.0	108	1	KV1M_HUMAN	P01605 homo sapien
4	419.5	74.6	108	1	KV1A_HUMAN	P01593 homo sapien
5	419.5	74.6	108	1	KV1P_HUMAN	P01608 homo sapien
6	419.5	74.6	108	1	KV1Y_HUMAN	P80362 homo sapien
7	413.5	73.6	108	1	KV1Q_HUMAN	P01609 homo sapien
8	409.5	72.9	129	1	KV1W_HUMAN	P04431 homo sapien
9	409	72.8	107	1	KV1D_HUMAN	P01596 homo sapien
10	408.5	72.7	108	1	KV1R_HUMAN	P01610 homo sapien
11	402.5	71.6	108	1	KV1H_HUMAN	P01600 homo sapien
12	397.5	70.7	108	1	KV1F_HUMAN	P01598 homo sapien
13	396.5	70.6	108	1	KV1V_HUMAN	P04430 homo sapien
14	390.5	69.5	108	1	KV1K_HUMAN	P01603 homo sapien
15	388.5	69.1	108	1	KV1E_HUMAN	P01597 homo sapien
16	386.5	68.8	108	1	KV1L_HUMAN	P01604 homo sapien
17	385.5	68.6	108	1	KV1N_HUMAN	P01606 homo sapien
18	384.5	68.4	108	1	KV1C_HUMAN	P01595 homo sapien
19	383.5	68.2	108	1	KV1G_HUMAN	P01599 homo sapien
20	383.5	68.2	129	1	KV1X_HUMAN	P04432 homo sapien
21	381.5	67.9	108	1	KV1S_HUMAN	P01611 homo sapien
22	376.5	67.0	134	1	KV4C_HUMAN	P06314 homo sapien
23	371.5	66.1	108	1	KV5J_MOUSE	P01643 mus musculu
24	368	65.5	117	1	KV1J_HUMAN	P01602 homo sapien
25	366.5	65.2	128	1	KV5E_MOUSE	P01637 mus musculu
26	365	64.9	133	1	KV4B_HUMAN	P06313 homo sapien
27	364.5	64.9	108	1	KV5O_MOUSE	P01648 mus musculu
28	363.5	64.7	108	1	KV5N_MOUSE	P01647 mus musculu
29	362	64.4	109	1	KV1T_HUMAN	P01612 homo sapien
30	362	64.4	117	1	KV1I_HUMAN	P01601 homo sapien
31	361.5	64.3	108	1	KV5K_MOUSE	P01644 mus musculu
32	359.5	64.0	108	1	KV5M_MOUSE	P01646 mus musculu
33	358.5	63.8	108	1	KV5L_MOUSE	P01645 mus musculu
34	356.5	63.4	112	1	KV1U_HUMAN	P01613 homo sapien
35	348.5	62.0	114	1	KV4A_HUMAN	P01625 homo sapien
36	348	61.9	129	1	KV3H_HUMAN	P04207 homo sapien
37	346	61.6	129	1	KV3M_HUMAN	P18136 homo sapien
38	345.5	61.5	108	1	KV5T_MOUSE	P01653 mus musculu
39	345	61.4	115	1	KV5F_MOUSE	P01638 mus musculu
40	341.5	60.8	108	1	KV5Q_MOUSE	P01650 mus musculu
41	341	60.7	109	1	KV3E_HUMAN	P01623 homo sapien
42	340.5	60.6	108	1	KV5S_MOUSE	P01652 mus musculu
43	339.5	60.4	108	1	KV5U_MOUSE	P04946 mus musculu
44	339	60.3	109	1	KV3D_HUMAN	P01622 homo sapien
45	339	60.3	109	1	KV3F_HUMAN	P01624 homo sapien

ALIGNMENTS

```
RESULT   1
KV1O_HUMAN
ID   KV1O_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION REI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei.); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01873; K1HURE.
DR   PDB; 1REI; 17-FEB-84.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
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FT   TURN          50     52
FT   STRAND        53     54
FT   TURN          56     57
FT   TURN          60     61
FT   STRAND        62     67
FT   TURN          68     69
FT   STRAND        70     75
FT   HELIX         80     82
FT   STRAND        85     90
FT   STRAND        98     98
FT   STRAND       102    106
FT   NON_TER      108    108
SQ   SEQUENCE   108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;


  Query Match             78.9%;  Score 443.5;  DB 1;  Length 108;
  Best Local Similarity   81.1%;  Pred. No. 5.7e-40;
  Matches   86;  Conservative    9;  Mismatches   10;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||: |||| ||: ||||||||||:|||:  | || |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQTPGKAPKLLIYEASNLQAGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEI 105
           |||||||| |||||||||||||||||| || :| :|||||||::|
Db      61 RFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQI 106


RESULT   2
KV1B_HUMAN
ID   KV1B_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the
RT   Bence-Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
CC       MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
CC       REGION OF THE KAPPA CHAIN REI.
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01862; K1HUAU.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11939 MW;  E8011187EE6F6FB9 CRC64;


  Query Match             78.2%;  Score 439.5;  DB 1;  Length 108;
  Best Local Similarity   79.4%;  Pred. No. 1.5e-39;
  Matches   85;  Conservative    8;  Mismatches   13;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||: |||| |: |||| |||||:|||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDISDYLNWYQQKPGKAPKLLIYDASNLESGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||| |||  :|||||||||||||||||| ||| | ||||||||||||
Db      61 RFSGGGSGAHFTFTISSLQPEDIATYYCQQYDYLPWTFGQGTKVEIK 107


RESULT   3
KV1M_HUMAN
ID   KV1M_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01605;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION LAY.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=77038198; PubMed=824717;
RA   Capra J.D., Klapper D.G.;
RT   "Complete amino acid sequence of the variable domains of two human
RT   IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT   specificities.";
RL   Scand. J. Immunol. 5:677-684(1976).
CC   -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC       CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC       WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC       GLOBULIN ACTIVITY.
DR   PIR; A01871; K1HULY.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  739993A95431434A CRC64;


  Query Match             75.0%;  Score 421.5;  DB 1;  Length 108;
  Best Local Similarity   75.0%;  Pred. No. 1.2e-37;
  Matches   81;  Conservative   11;  Mismatches   13;  Indels    3;  Gaps    2;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||| ||||||||||: ||::| |: |||| || ||:|||:  |  : |:||
Db       1 DIQMTQSPSSLSVSVGDRVTITCQASQNVNAYLNWYQQKPGLAPKLLIYGASTREAGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
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          |||||||| |:|||||||||||||||| ||:| |  |||||||||:|
Db     61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYNN-WPPTFGQGTKVEVK 107


RESULT   4
KV1A_HUMAN
ID   KV1A_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01593;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION AG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=69234734; PubMed=4893682;
RA   Titani K., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT   complete sequence and the location of the disulfide bridges.";
RL   J. Biol. Chem. 244:3550-3560(1969).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01861; K1HUAG.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11992 MW;  E3B3B246C18F0C4F CRC64;


  Query Match             74.6%;  Score 419.5;  DB 1;  Length 108;
  Best Local Similarity   76.6%;  Pred. No. 1.9e-37;
  Matches   82;  Conservative    9;  Mismatches   15;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: ||||| |: |||| | |||::||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDINHYLNWYQQGPKKAPKILIYDASNLETGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||| | |:||||| |||||||||| ||| |  |||||||:|||
Db      61 RFSGSGFGTDFTFTISGLQPEDIATYYCQQYDTLPRTFGQGTKLEIK 107


RESULT   5
KV1P_HUMAN
ID   KV1P_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01608;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION ROY.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=68362076; PubMed=5595110;
RA   Hilschmann N.;
RT   "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT   Cum.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN   [2]
RP   REVISIONS TO 39 AND 41.
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RL   (In) Franek F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press,
RL   New York (1969).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01874; K1HURY.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11782 MW;  F5ACEDE5A313DF3A CRC64;


  Query Match             74.6%;  Score 419.5;  DB 1;  Length 108;
  Best Local Similarity   75.7%;  Pred. No. 1.9e-37;
  Matches   81;  Conservative   12;  Mismatches   13;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: |||| :: |||| |||||:|||:  | |: |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCQASQDISIFLNWYQQKPGKAPKLLIYDASKLEAGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           ||||:||| |:|||||||||||||||| |:|||  ||| ||||: |
Db      61 RFSGTGSGTDFTFTISSLQPEDIATYYCQQFDNLPLTFGGGTKVDFK 107


RESULT   6
KV1Y_HUMAN
ID   KV1Y_HUMAN     STANDARD;      PRT;   108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=95086080; PubMed=7993911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
RN   [2]
RP   SEQUENCE OF 1-35.
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human kI Bence Jones protein Wat.";
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RL   J. Mol. Biol. 147:185-193(1981).
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PDB; 1WTL; 01-NOV-94.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   CONFLICT     30     31       TN -> SD (IN REF. 2).
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11737 MW;  D9D941B3F0FAE697 CRC64;


  Query Match             74.6%;  Score 419.5;  DB 1;  Length 108;
  Best Local Similarity   75.7%;  Pred. No. 1.9e-37;
  Matches   81;  Conservative   11;  Mismatches   14;  Indels    1;  Gaps    1;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||||||||||||||||||||||: |||| |: |:|| ||:||::||:  | |: |:||
Db      1 DIQMTQSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPS 60

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          |||||||| |:|||||||||||||||| ||| |  ||| ||||:||
Db     61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDTLPLTFGGGTKVDIK 107


RESULT   7
KV1Q_HUMAN
ID   KV1Q_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01609;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION SCW.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75059271; PubMed=4435756;
RA   Eulitz M., Hilschmann N.;
RT   "The primary structure of a human immunoglobulin L-chain of
RT   kappa-type (Bence-Jones protein Scw.), II: The chymotryptic peptides
RT   and the complete amino acid sequence.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01875; K1HUSW.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11764 MW;  32CECDDDF9644414 CRC64;


  Query Match             73.6%;  Score 413.5;  DB 1;  Length 108;
  Best Local Similarity   74.8%;  Pred. No. 8.1e-37;
  Matches   80;  Conservative   10;  Mismatches   16;  Indels    1;  Gaps    1;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||||||||||||||||||||||: |||| |:: || | |||||||||:  | |: |:||
Db      1 DIQMTQSPSSLSASVGDRVTITCQASQDIRKHLNWYDQKPGKAPRLLIYGASTLETGVPS 60

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
          |||||||| |:| |||:|||||| ||| ||||:  ||||||:|| |
Db     61 RFSGSGSGTDFTLTISTLQPEDIGNYYCQQYDNVPITFGQGTRVENK 107


RESULT   8
KV1W_HUMAN
ID   KV1W_HUMAN     STANDARD;      PRT;   129 AA.
AC   P04431;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X00965; CAA25477.1; ALT_TERM.
DR   PIR; A01883; K1HUWK.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       IG KAPPA CHAIN V-I REGION WALKER.
FT   DOMAIN       23     45       FRAMEWORK 1.
FT   DOMAIN       46     56       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       57     71       FRAMEWORK 2.
FT   DOMAIN       72     78       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       79    110       FRAMEWORK 3.
FT   DOMAIN      111    119       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      120    129       FRAMEWORK 4.
FT   DISULFID     45    110       BY SIMILARITY.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14069 MW;  F941FA07D4AFC2F9 CRC64;


  Query Match             72.9%;  Score 409.5;  DB 1;  Length 129;
  Best Local Similarity   74.8%;  Pred. No. 2.6e-36;
  Matches   80;  Conservative   10;  Mismatches   16;  Indels    1;  Gaps    1;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          |||||||||||||||||||||||: || |: |: |||| |||||:|||:  |:|| |: |
Db     23 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPKLLIYAASSLQSGVTS 82
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Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
           |||||||| |:| ||||||||| ||||| | |  | ||||||::|||
Db      83 RFSGSGSGTDFTLTISSLQPEDSATYYCQQSYSTLITFGQGTRLEIK 129


RESULT  9
KV1D_HUMAN
ID   KV1D_HUMAN     STANDARD;      PRT;   107 AA.
AC   P01596;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION CAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=75075135; PubMed=4216454;
RA   Milstein C.P., Deverson E.V.;
RT   "Primary structure of kappa light chain from a human myeloma
RT   protein.";
RL   Eur. J. Biochem. 49:377-391(1974).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC       MARKER.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01864; K1HUAR.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Glycoprotein.
FT   CARBOHYD     28     28       N-LINKED (GLCNAC. . .).
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11703 MW;  E1BF0DF9844C3346 CRC64;


  Query Match             72.8%;  Score 409;  DB 1;  Length 107;
  Best Local Similarity   68.9%;  Pred. No. 2.4e-36;
  Matches   73;  Conservative   20;  Mismatches   13;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||:|||||||| ||| ||:|: ::||||| ||||::||: :|:|: |:||
Db       1 DIQMTQSPSTLSASVGDRVAITCRASQNISSWLAWYQQKPGKAPKVLIYKSSSLESGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||| |:| |||||:|:: ||||| ||:  :||| ||||:||
Db      61 RFSGSGSGTDFTLTISSLZPBBFATYYCQQYNTFFTFGPGTKVDIK 106


RESULT  10
KV1R_HUMAN
ID   KV1R_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01610;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION WEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=83273707; PubMed=6410398;
RA   Goni F., Frangione B.;
RT   "Amino acid sequence of the Fv region of a human monoclonal IgM
RT   (protein WEA) with antibody activity against 3,4-pyruvylated
RT   galactose in Klebsiella polysaccharides K30 and K33.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC   -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC       AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC       WALDENSTROM'S MACROGLOBULINEMIA.
DR   PIR; A01876; K1HUWE.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Monoclonal antibody.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11840 MW;  9249B61F0945618C CRC64;


  Query Match             72.7%;  Score 408.5;  DB 1;  Length 108;
  Best Local Similarity   72.0%;  Pred. No. 2.7e-36;
  Matches   77;  Conservative   12;  Mismatches   17;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: || |   : |||| || ||: ||:  ::|| |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLTWYQQKPGTAPKRLIYGATSLQSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| ::| ||:|||||| |||||||| :  ||||||||||:|
Db      61 RFSGSGSGTEFTLTINSLQPEDFATYYCLQYSSFPWTFGQGTKVEVK 107


RESULT  11
KV1H_HUMAN
ID   KV1H_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01600;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION HAU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71032830; PubMed=4097974;
RA   Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT   chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT   subgroups.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01868; K1HUHU.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
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SQ   SEQUENCE   108 AA;  11671 MW;  08D3A6160D8D0618 CRC64;

  Query Match             71.6%;  Score 402.5;  DB 1;  Length 108;
  Best Local Similarity   72.9%;  Pred. No. 1.2e-35;
  Matches   78;  Conservative   12;  Mismatches   16;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: || |: |::|||| |||||::||:  |:|  |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLSWYQQKPGKAPQVLIYAASSLPSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
           |||||||| |:| ||||||||| ||||| | |    :|||||:||||
Db      61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQNYITPTSFGQGTRVEIK 107


RESULT  12
KV1F_HUMAN
ID   KV1F_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01598;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION EU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=71064023; PubMed=5489770;
RA   Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT   acid sequence of the light chain.";
RL   Biochemistry 9:3155-3161(1970).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC   -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR   PIR; A01866; K1HUEU.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11788 MW;  9CD294F2F4D88823 CRC64;

  Query Match             70.7%;  Score 397.5;  DB 1;  Length 108;
  Best Local Similarity   70.1%;  Pred. No. 3.9e-35;
  Matches   75;  Conservative   16;  Mismatches   15;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||:|||||||||||||: || || ::||||| |||||:||::  |:|: |:||
Db       1 DIQMTQSPSTLSASVGDRVTITCRASQSINTWLAWYQQKPGKAPKLLMYKASSLESGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYD-NLWTFGQGTKVEIK 106
           || ||||| ::| |||||||:| ||||| ||: :   ||||||||:|
Db      61 RFIGSGSGTEFTLTISSLQPDDFATYYCQQYNSDSKMFGQGTKVEVK 107


RESULT  13
KV1V_HUMAN
ID   KV1V_HUMAN     STANDARD;      PRT;   108 AA.
AC   P04430;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION BAN.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=86174817; PubMed=3083240;
RA   Dwulet F.E., O'Connor T.P., Benson M.D.;
RT   "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL   Mol. Immunol. 23:73-78(1986).
DR   PIR; A01878; K1HUBN.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Amyloid.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11840 MW;  CD3FD944FE96FD37 CRC64;

  Query Match             70.6%;  Score 396.5;  DB 1;  Length 108;
  Best Local Similarity   70.1%;  Pred. No. 5e-35;
  Matches   75;  Conservative   14;  Mismatches   17;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||:|||||||||||||||||||: || :  |:||:|| |||||: ||:  | || |:||
Db       1 DIQLTQSPSSLSASVGDRVTITCRASQSVYNYVAWFQQKPGKAPKSLIYDASTLQSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
             |:||||| |:  |||||||||| ||||| ||::  :|||||||||:||
Db      61 NFTGSGSGTDFILTISSLQPEDFATYYCQQYNSYPYTFGQGTKVQIK 107


RESULT  14
KV1K_HUMAN
ID   KV1K_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01603;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION KA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=76189985; PubMed=818073;
RA   Shinoda T.;
RT   "Comparative structural studies on the light chains of human
RT   immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL   J. Biochem. 77:1277-1296(1975).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
```

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CC   -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR   PIR; A01869; K1HUKA.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region; Bence-Jones protein.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11900 MW;  768839FBED5A2F4B CRC64;


  Query Match             69.5%;  Score 390.5;  DB 1;  Length 108;
  Best Local Similarity   66.4%;  Pred. No. 2.1e-34;
  Matches   71;  Conservative   19;  Mismatches   16;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||:|| |||||||||: || :  |: |||| |||||:|||:  |:|: |:||
Db       1 DIQMTQSPSTLSVSVGDRVTITCEASQTVLSYLNWYQQKPGKAPKLLIYAASSLETGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||| ||| ::||||||::|:: ||||| :| :|  ||||||||::|
Db      61 RFSGQGSGTBFTFTISSVZPZBFATYYCQZYLDLPRTFGQGTKVDLK 107


RESULT  15
KV1E_HUMAN
ID   KV1E_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01597;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   IG KAPPA CHAIN V-I REGION DEE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=72053133; PubMed=5124396;
RA   Milstein C.P., Deverson E.V.;
RT   "The amino acid sequence of a human kappa light chain.";
RL   Biochem. J. 123:945-958(1971).
CC   -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR   PIR; A01865; K1HUDE.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   Immunoglobulin V region.
FT   DOMAIN        1     23       FRAMEWORK 1.
FT   DOMAIN       24     34       COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN       35     49       FRAMEWORK 2.
FT   DOMAIN       50     56       COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN       57     88       FRAMEWORK 3.
FT   DOMAIN       89     97       COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN       98    107       FRAMEWORK 4.
FT   DISULFID     23     88       BY SIMILARITY.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11661 MW;  BDD6E350017F1E51 CRC64;


  Query Match             69.1%;  Score 388.5;  DB 1;  Length 108;
  Best Local Similarity   68.9%;  Pred. No. 3.4e-34;
  Matches   73;  Conservative   13;  Mismatches   19;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           :|:|||||||||||||||||||:  | :|||: |||| |||||::||   |:|: |:||
Db       1 BIZMTQSPSSLSASVGDRVTITCRAGQSVNKYLNWYQQKPGKAPKVLIFAASSLKSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEI 105
           |||||||| |:| ||| | ||| ||||| | |   :||| |||||:
Db      61 RFSGSGSGTDFTLTISGLLPEDFATYYCQQSYTTPYTFGPGTKVEM 106


Search completed: May  7, 2002, 12:32:34
Job time: 565 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 7, 2002, 12:31:42 ; Search time 67.26 Seconds
(without alignments)
230.521 Million cell updates/sec

Title: US-09-155-739-7
Perfect score: 562
Sequence: 1 DIQMTQSPSSLSASVGDRVT.....YCLQYDNLWTFGQGTKVEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	428.5	76.2	108	4	Q9UL77	Q9ul77 homo sapien
2	406.5	72.3	108	4	Q9UL70	Q9ul70 homo sapien
3	395	70.3	107	4	Q9UL81	Q9ul81 homo sapien
4	385.5	68.6	108	4	Q9UL79	Q9ul79 homo sapien
5	384.5	68.4	214	11	Q9R1A5	Q9r1a5 mus musculu
6	362.5	64.5	107	11	Q9JL84	Q9j184 mus musculu
7	337.5	60.1	298	11	Q9QYF0	Q9qyf0 mus musculu
8	336.5	59.9	108	4	Q9UL83	Q9ul83 homo sapien
9	332	59.1	109	4	Q9UL85	Q9ul85 homo sapien
10	331	58.9	109	4	Q9UL78	Q9ul78 homo sapien
11	329	58.5	109	4	Q9UL86	Q9ul86 homo sapien
12	307.5	54.7	107	11	Q9ERZ9	Q9erz9 mus musculu
13	302.5	53.8	99	11	Q9JL74	Q9jl74 mus musculu
14	297	52.8	106	5	Q9U410	Q9u410 schistosoma
15	294	52.3	238	11	Q99M37	Q99m37 mus musculu
16	292.5	52.0	114	4	Q9UL80	Q9ul80 homo sapien
17	284.5	50.6	101	11	Q9JL78	Q9jl78 mus musculu
18	281.5	50.1	97	11	Q9JL76	Q9jl76 mus musculu
19	273.5	48.7	109	6	Q9N0W5	Q9n0w5 oryctolagus
20	269.5	48.0	103	11	Q9JL80	Q9jl80 mus musculu
21	255	45.4	104	11	Q9JL82	Q9jl82 mus musculu
22	212.5	37.8	107	4	Q9UL82	Q9ul82 homo sapien
23	206	36.7	107	4	Q9NSD6	Q9nsd6 homo sapien
24	183	32.6	109	11	Q9ET13	Q9et13 mus musculu
25	170	30.2	130	4	Q9NP29	Q9np29 homo sapien
26	168	29.9	235	11	Q99M11	Q99m11 mus musculu
27	165	29.4	337	13	Q9IB02	Q9ib02 sphoeroides
28	141.5	25.2	135	4	Q9H5Z4	Q9h5z4 homo sapien
29	141	25.1	342	13	Q9IB00	Q9ib00 sphoeroides
30	132.5	23.6	93	4	Q9UL76	Q9ul76 homo sapien
31	125	22.2	334	13	Q9IB05	Q9ib05 sphoeroides
32	124	22.1	123	11	Q61243	Q61243 mus musculu
33	115	20.5	339	13	Q9IAY8	Q9iay8 sphoeroides
34	110	19.6	339	13	Q9IAZ1	Q9iaz1 sphoeroides
35	109.5	19.5	118	11	Q9Z1C4	Q9z1c4 mus musculu
36	109.5	19.5	169	4	Q9Y2N4	Q9y2n4 homo sapien
37	109	19.4	326	13	Q9IAY7	Q9iay7 sphoeroides
38	109	19.4	473	11	Q9D8L4	Q9d814 mus musculu
39	108.5	19.3	118	4	Q9UL91	Q9ul91 homo sapien
40	108	19.2	332	13	Q9IB08	Q9ib08 sphoeroides
41	108	19.2	339	13	Q9IAZ7	Q9iaz7 sphoeroides
42	107.5	19.1	118	4	Q9UL72	Q9ul72 homo sapien
43	107	19.0	341	13	Q9IB06	Q9ib06 sphoeroides
44	106	18.9	326	13	Q9IAZ5	Q9iaz5 sphoeroides
45	106	18.9	509	11	Q9QX57	Q9qx57 mus musculu

ALIGNMENTS

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RESULT   1
Q9UL77
ID   Q9UL77      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035037; AAD56273.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11738 MW;  C06681716C4D16F3 CRC64;


  Query Match             76.2%;  Score 428.5;  DB 4;  Length 108;
  Best Local Similarity   76.6%;  Pred. No. 3.3e-40;
  Matches   82;  Conservative    8;  Mismatches   16;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: || |: |: |||| ||||| |||:  |:|| |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
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          |||||||| |:| ||||||||| ||||| | |   ||||:|||||||
Db      61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTSWTFGEGTKVEIK 107


RESULT   2
Q9UL70
ID   Q9UL70      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035044; AAD56280.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11633 MW;  B7BEDC3E41FCCA37 CRC64;


  Query Match             72.3%;  Score 406.5;  DB 4;  Length 108;
  Best Local Similarity   72.9%;  Pred. No. 9.3e-38;
  Matches   78;  Conservative   12;  Mismatches   16;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: || |: |:||||| ||| |: ||:  | || |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKSLIYAASTLQSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| |:| |||||||||:||||| :|::   ||| |||:|||
Db      61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107


RESULT   3
Q9UL81
ID   Q9UL81      PRELIMINARY;      PRT;   107 AA.
AC   Q9UL81;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035033; AAD56269.1; -.
DR   HSSP; P80362; 1WTL.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11501 MW;  070549FDE0754748 CRC64;


  Query Match             70.3%;  Score 395;  DB 4;  Length 107;
  Best Local Similarity   71.7%;  Pred. No. 1.7e-36;
  Matches   76;  Conservative   10;  Mismatches   20;  Indels    0;  Gaps    0;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||||||||||||||||||||: || |: |: |||| ||||| |||:  |:|| |:||
Db       1 DIQMTQSPSSLSASVGDRVTITCRASQSISNYLNWYQQKPGKAPNLLIYAASSLQSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLWTFGQGTKVEIK 106
           |||||||| |:| ||| || || ||||| |  :  ||| ||||:|:
Db      61 RFSGSGSGTDFTLTISGLQAEDFATYYCQQSYSALTFGPGTKVDIR 106


RESULT   4
Q9UL79
ID   Q9UL79      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035035; AAD56271.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11787 MW;  DB5845F19724FB4E CRC64;


  Query Match             68.6%;  Score 385.5;  DB 4;  Length 108;
  Best Local Similarity   72.0%;  Pred. No. 2e-35;
  Matches   77;  Conservative    8;  Mismatches   21;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           || |||||| |||| ||||||:|: || |: |:||||| ||||| |||:  | || |:||
Db       1 DIVMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAASTLQSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| |:| ||| || || ||||| || :   ||||||||||
Db      61 RFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFPPTFGQGTKVEIK 107


RESULT   5
Q9R1A5
ID   Q9R1A5      PRELIMINARY;      PRT;   214 AA.
AC   Q9R1A5;
```

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DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT   "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT   antibody (Mab 7, its light and heavy chains) and construction of a
RT   single chain antibody (scFV).";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF152371; AAD40242.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   SMART; SM00410; IG_like; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT   NON_TER       1      1
FT   NON_TER     214    214
SQ   SEQUENCE   214 AA;  23922 MW;  52BA205FDE995E2A CRC64;
```

```
  Query Match             68.4%;  Score 384.5;  DB 11;  Length 214;
  Best Local Similarity   66.4%;  Pred. No. 5.7e-35;
  Matches   71;  Conservative   18;  Mismatches   17;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||:||||||: ||:|:|||||||| ||||| |::|:|| |||:|: ||:  : |  |:||
Db       1 DIQLTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           ||||||||:||: ||||| ||:  ||||||   :||| |||:|||
Db      61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPFTFGSGTKLEIK 107
```

```
RESULT   6
Q9JL84
ID   Q9JL84      PRELIMINARY;      PRT;   107 AA.
AC   Q9JL84;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206022; AAF69320.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11648 MW;  ACF9B1253ACA1E5D CRC64;
```

```
  Query Match             64.5%;  Score 362.5;  DB 11;  Length 107;
  Best Local Similarity   65.4%;  Pred. No. 7.2e-33;
  Matches   70;  Conservative   11;  Mismatches   25;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           |||||| ||||||:|||   |  || |:    |:|| |    :|||:|||:|  |:||
Db       1 DIQMTQSTSSLSASLGDRVXXXCSASQGISNXXXWFQQKPDGTVKLLIYYTSSLXSGVPS 60

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||||| ||: |||:|:|||||||||| ||    |||| |||:|||
Db      61 RFSGSGSGXDYSLTISNLEPEDIATYYCQQYSKFPWTFGGGTKLEIK 107
```

```
RESULT   7
Q9QYF0
ID   Q9QYF0      PRELIMINARY;      PRT;   298 AA.
AC   Q9QYF0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CN 8 SCFV.
GN   CN 8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=SPLEEN;
RA   Shinohara N., Demura T., Fukuda H.;
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=SPLEEN;
RA   shinohara N., Demura T., Fukuda H.;
RT   "Isolation of a novel type of vascular cell wall-specific monoclonal
RT   antibody recognizing a cell polarity using a phage display subtraction
RT   method.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AB036341; BAA88633.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 2.
SQ   SEQUENCE   298 AA;  31867 MW;  E0F96B8A17004317 CRC64;
```

```
  Query Match             60.1%;  Score 337.5;  DB 11;  Length 298;
  Best Local Similarity   58.9%;  Pred. No. 1.4e-29;
  Matches   63;  Conservative   19;  Mismatches   24;  Indels    1;  Gaps    1;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
           ||::||||:|||||||: |||||: | :|: |:|||||  ||:|:||::    |  |:||
Db     173 DIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGVPS 232

Qy      61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
           ||||||||  |:  |:||||||  :|||  :    :||| |||:|||
Db     233 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWTTPYTFGGGTKLEIK 279
```

```
RESULT   8
Q9UL83
ID   Q9UL83      PRELIMINARY;      PRT;   108 AA.
AC   Q9UL83;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
```

```
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035031; AAD56267.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  9F9C5A92EBA96EEA CRC64;


  Query Match             59.9%;  Score 336.5;  DB 4;  Length 108;
  Best Local Similarity   60.2%;  Pred. No. 5.6e-30;
  Matches   65;  Conservative   17;  Mismatches   23;  Indels    3;  Gaps    2;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          :| |||||::|| | |:| |::|: || ::  :||||| ||:||||||:  |    |||:
Db      1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYCASTRATGIPA 60

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW--TFGQGTKVEIK 106
          |||||||| ::| |||||| || | |||  |:| |  ||| ||||:||
Db     61 RFSGSGSGTEFTLTISSLQFEDFAVYYCQHYNN-WPFTFGPGTKVDIK 107


RESULT   9
Q9UL85
ID   Q9UL85      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL85;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035029; AAD56265.1; -.
DR   HSSP; P01607; 1REI.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11761 MW;  FB1E43E7C7AFACCC CRC64;


  Query Match             59.1%;  Score 332;  DB 4;  Length 109;
  Best Local Similarity   61.5%;  Pred. No. 1.8e-29;
  Matches   67;  Conservative   14;  Mismatches   24;  Indels    4;  Gaps    2;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPS 60
          :| |||||::|| | |:| |::|  || |:  :||||| ||:||||||:  |    |||:
Db      1 EIVMTQSPATLSVSPGERATLSCWASQSISSNLAWYQQKPGQAPRLLIYGASTRATGIPA 60

Qy     61 RFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNLW---TFGQGTKVEIK 106
          |||||||| ::| |||||| || | |:| || | |   ||| |||||||
Db     61 RFSGSGSGTEFTLTISSLQSEDFAIYHCQQY-NSWPPLTFGGGTKVEIK 108


RESULT  10
Q9UL78
ID   Q9UL78      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035036; AAD56272.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11646 MW;  5F675C52EC7EE197 CRC64;


  Query Match             58.9%;  Score 331;  DB 4;  Length 109;
  Best Local Similarity   60.2%;  Pred. No. 2.3e-29;
  Matches   65;  Conservative   16;  Mismatches   25;  Indels    2;  Gaps    2;

Qy      1 DIQMTQSPSSLSASVGDRVTITCKTSQDI-NKYMAWYQQTPGKAPRLLIHYTSALQPGIP 59
          :| :|||| :|| | |:| |::|: || : : |:||||| ||:||||||:  |:   |||
Db      1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGIP 60

Qy     60 SRFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
          ||||||||  |:| ||| |:||| | ||| ||  :  ||| |||||||
Db     61 DRFSGSGSGTDFTLTISRLEPEDCAVYYCQQYGSSPLTFGGGTKVEIK 108


RESULT  11
Q9UL86
ID   Q9UL86      PRELIMINARY;      PRT;   109 AA.
AC   Q9UL86;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98277139; PubMed=9614934;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
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```
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF035028; AAD56264.1; -.
DR   HSSP; P01789; 1MCP.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     109     109
SQ   SEQUENCE   109 AA;  11928 MW;  243325F72C7DAC83 CRC64;


  Query Match             58.5%;  Score 329;  DB 4;  Length 109;
  Best Local Similarity   58.3%;  Pred. No. 3.9e-29;
  Matches   63;  Conservative   19;  Mismatches   24;  Indels    2;  Gaps    2;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDI-NKYMAWYQQTPGKAPRLLIHYTSALQPGIP 59
           :| :|||| :||   |:| |::|: || : : |:|||| ||:|||||: ||:   |||
Db       1 EIVLTQSPGTLSLFPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGTSSRATGIP 60

Qy      60 SRFSGSGSGRDYTFTISSLQPEDIATYYCLQY-DNLWTFGQGTKVEIK 106
             ||||||| |:| ||| |:||| | ||| ||  :::||| ||||:||
Db      61 DRFSGSGSETDFTLTISRLEPEDFAVYYCQQYGSSIFTFGPGTKVDIK 108


RESULT  12
Q9ERZ9
ID   Q9ERZ9      PRELIMINARY;      PRT;   107 AA.
AC   Q9ERZ9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT   "Cloning and sequencing of the light chain fragment of variable region
RT   genes of an anti-hTNF-a monoclonal antibody.";
RL   J. Cell. Mol. Immunol. 12:21-26(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT   "Construction and sequencing of the single-chain antibody gene of a
RT   human TNF-alpha specific monoclonal antibody.";
RL   Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF262753; AAG23804.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER     107     107
SQ   SEQUENCE   107 AA;  11784 MW;  2B15EEA6604A26C3 CRC64;


  Query Match             54.7%;  Score 307.5;  DB 11;  Length 107;
  Best Local Similarity   53.3%;  Pred. No. 9.3e-27;
  Matches   57;  Conservative   21;  Mismatches   22;  Indels    7;  Gaps    2;

Qy       4 MTQSPSSLSASVGDRVTITCKTSQDI------NKYMAWYQQTPGKAPRLLIHYTSALQPG 57
           |||||||: ||| :||::||:|| :        |:|||: ||::| ||::: |  : |
Db       1 MTQSPSSLAMSVGQKVTMSCKSSQSVLNSNTQKNYLAWYQKKPGQSPELLVYFASTRESG 60

Qy      58 IPSRFSGSGSGRDYTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKV 103
           :| || ||||| |:| ||||:| ||:| |:| | |   :||| |||:
Db      61 VPDRFMGSGSGTDFTLTISSVQTEDLADYFCQQHYRTPFTFGSGTKL 107


RESULT  13
Q9JL74
ID   Q9JL74      PRELIMINARY;      PRT;    99 AA.
AC   Q9JL74;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
RT   acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF206032; AAF69330.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER      99      99
SQ   SEQUENCE   99 AA;  10939 MW;  3B25D0E784533324 CRC64;


  Query Match             53.8%;  Score 302.5;  DB 11;  Length 99;
  Best Local Similarity   58.8%;  Pred. No. 3.1e-26;
  Matches   57;  Conservative   16;  Mismatches   23;  Indels    1;  Gaps    1;

Qy      11 LSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPSRFSGSGSGRD 70
           |  | |||||||||| || ::  :||||| ||::|:|||:| |    |:| ||:||| | |
Db       3 LLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGYGTD 62

Qy      71 YTFTISSLQPEDIATYYCLQ-YDNLWTFGQGTKVEIK 106
           :|||||::| ||:| |:| | | :  ||| |||:|||
Db      63 FTFTISTVQAEDLAVYFCQQDYSSPRTFGGGTKLEIK 99


RESULT  14
Q9U410
ID   Q9U410      PRELIMINARY;      PRT;   106 AA.
AC   Q9U410;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE   VARIABLE REGION (FRAGMENT).
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Neodermata;
OC   Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae;
OC   Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT   "Amplification, cloning and sequence analysis of the light chain
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RT   variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT   Schistosoma japonicum.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; AF207620; AAF19434.1; -.
DR   HSSP; P01679; 2FBJ.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
FT   NON_TER       1       1
FT   NON_TER     106     106
SQ   SEQUENCE   106 AA;  11478 MW;  F20F544426BAE63E CRC64;


  Query Match             52.8%;  Score 297;  DB 5;  Length 106;
  Best Local Similarity   54.8%;  Pred. No. 1.3e-25;
  Matches   57;  Conservative   20;  Mismatches   25;  Indels    2;  Gaps    2;

Qy       4 MTQSPSSLSASVGDRVTITCKTSQDINKYMAWYQQTPGKAPRLLIHYTSALQPGIPSRFS 63
           :||||: :||| |::||:||  |  :: |: || | || :|||||: || |  |:| |||
Db       4 LTQSPAIMSASPGEKVTMTCSASSSVS-YVYWYLQKPGSSPRLLIYDTSNLASGVPVRFS 62

Qy      64 GSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
           |||||  |: ||| :: || ||||| |: :  :||| |||:|:|
Db      63 GSGSGTSYSLTISRMEAEDAATYYCQQWTSYPFTFGSGTKLELK 106


RESULT  15
Q99M37
ID   Q99M37      PRELIMINARY;      PRT;   238 AA.
AC   Q99M37;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   UNKNOWN (PROTEIN FOR MGC:5947).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY TUMOR;
RA   Strausberg R.;
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC002035; AAH02035.1; -.
SQ   SEQUENCE   238 AA;  26344 MW;  FB2B06A0B801330A CRC64;


  Query Match             52.3%;  Score 294;  DB 11;  Length 238;
  Best Local Similarity   50.0%;  Pred. No. 7.4e-25;
  Matches   56;  Conservative   22;  Mismatches   28;  Indels    6;  Gaps    2;

Qy       1 DIQMTQSPSSLSASVGDRVTITCKTSQDI-----NKYMAWYQQTPGKAPRLLIHYTSALQ 55
           |: |||:| ||  |:||: :|:|::|| |     | |: || | ||::|:|||:  |
Db      20 DVVMTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 79

Qy      56 PGIPSRFSGSGSGRDYTFTISSLQPEDIATYYCLQYDNL-WTFGQGTKVEIK 106
            |:| |||||||| |:|  || :: ||:  ||| |  :: :||| |||:|||
Db      80 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGSGTKLEIK 131


Search completed: May  7, 2002, 12:31:42
Job time: 628 sec
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